

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 11:06:42 ; Search time 135 Seconds  
(without alignments)  
329.178 Million cell updates/sec

Title: US-10-613-390b-1

Perfect score: 1 tatcaaggcgctggccctcata 25

Scoring table: IDENTITY NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1427136

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/1/COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5/COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A/COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B/COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H/COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS/COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP/COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RR/COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	69.6	25	US-09-396-196G-116728	Sequence 116728,
2	15.8	63.2	25	US-09-396-196G-116728	Sequence 116728,
3	14.8	59.2	25	US-09-396-196G-86335	Sequence 86335, A
4	14.8	59.2	25	US-09-396-196G-86336	Sequence 86336, A
5	14.4	57.6	70	US-08-434-001-117	Sequence 117, App
6	14.4	57.6	70	US-08-433-585-117	Sequence 117, App
7	14.4	57.6	70	US-08-434-425-117	Sequence 117, App
8	14.4	57.6	70	US-08-437-667-117	Sequence 117, App
9	14.4	57.6	70	US-08-906-955-117	Sequence 117, App
10	14.4	57.6	70	US-08-945-909-117	Sequence 117, App
11	14.4	57.6	70	US-09-396-002A-117	Sequence 117, App
12	14.4	57.6	70	US-10-077-319-117	Sequence 117, App
13	14.4	57.6	70	PCT-US96-06060-117	Sequence 117, App
14	14.2	56.8	25	US-09-396-196G-26177	Sequence 26177, A
15	14.2	56.8	49	US-08-171-389-405	Sequence 405, App
16	14.2	56.8	49	US-08-171-389-405	Sequence 405, App
17	14.2	56.8	49	US-08-123-936-405	Sequence 405, App
18	14.2	56.8	49	US-08-123-936-405	Sequence 405, App
19	14.2	56.8	49	US-08-475-228A-405	Sequence 405, App
20	14.2	56.8	49	US-08-475-228A-405	Sequence 405, App
21	14.2	56.8	49	US-08-482-080A-405	Sequence 405, App
22	14.2	56.8	49	US-08-482-080A-405	Sequence 405, App
23	14.2	56.8	49	US-09-354-947-405	Sequence 405, App
24	14.2	56.8	49	US-09-354-947-405	Sequence 405, App

25	14.2	56.8	49	3	US-09-993-346-405	Sequence 405, App
26	14.2	56.8	49	6	PCT-US93-12388-405	Sequence 405, App
27	14.2	56.8	49	6	PCT-US93-12388-405	Sequence 405, App
28	14.2	56.8	49	6	PCT-US93-12388-405	Sequence 405, App
29	14	56.0	63	3	US-09-508-516-4	Sequence 4, Appl1
30	13.8	55.2	61	3	US-09-513-999C-15155	Sequence 15155, A
31	13.4	53.6	50	3	US-10-131-827-7211	Sequence 7211, Ap
32	13.4	53.6	51	3	US-09-443-199C-1033	Sequence 1033, Ap
33	13.4	53.6	67	2	US-07-977-284A-245	Sequence 245, Ap
34	13.4	53.6	67	2	US-08-256-426B-245	Sequence 245, App
35	13.4	53.6	68	3	US-09-513-999C-23652	Sequence 23652, A
36	13.4	53.6	83	3	US-09-621-976-8355	Sequence 8355, Ap
37	13.2	52.8	25	3	US-09-396-196G-22105	Sequence 22105, A
38	13.2	52.8	25	3	US-09-396-196G-86335	Sequence 86335, A
39	13.2	52.8	25	3	US-09-396-196G-86336	Sequence 86336, A
40	13.2	52.8	25	3	US-09-396-196G-86335	Sequence 86335, A
41	13.2	52.8	28	2	US-08-331-394-46	Sequence 46, Appl1
42	13.2	52.8	28	2	US-08-331-394-51	Sequence 51, Appl1
43	13.2	52.8	28	2	US-08-250-858-46	Sequence 46, Appl1
44	13.2	52.8	28	2	US-08-250-858-51	Sequence 51, Appl1
45	13.2	52.8	28	2	US-08-446-915-46	Sequence 46, Appl1

## ALIGNMENTS

```
RESULT 1
US-09-396-196G-116728/c
; Sequence 116728, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-116728

Query Match      69.6%; Score 17.4; DB 3; Length 25;
Best Local Similarity 94.7%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AGGGGCTGGGCTTAAAT 24
        |||||
Db      25 AGGGGCTGGGCTTAAAT 7

RESULT 2
US-09-396-196G-116728
; Sequence 116728, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
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NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 116728  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-116728

Query Match  
Best Local Similarity 63.2%; Score 15.8; DB 3; Length 25;  
Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGGCCCCCT 20  
DB 7 ATTAAGTGCAGGCCCT 25

RESULT 3  
US-09-396-196G-86335  
Sequence 86335, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 86335  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-86335

Query Match  
Best Local Similarity 59.2%; Score 14.8; DB 3; Length 25;  
Pred. No. 3.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCCCTA 22  
DB 7 AAGAGCCTGGCCACTTA 24

RESULT 4  
US-09-396-196G-86336  
Sequence 86336, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 86336  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-86336

Query Match 59.2%; Score 14.8; DB 3; Length 25;

Best Local Similarity 88.9%; Pred. No. 3.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCCCTA 22  
DB 1 AAGAGCCTGGCCACTTA 18

RESULT 5  
US-08-434-001-117/c  
Sequence 117, Application US/08434001  
Patent No. 5712375  
GENERAL INFORMATION:  
APPLICANT: JENSEN, KIRK  
APPLICANT: CHEN, HANG  
APPLICANT: MORRIS, KEVIN  
APPLICANT: STEPHENS, ANDREW  
APPLICANT: GOLD, LARRY  
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE  
NUMBER OF INVENTIONS: SELEX  
NUMBER OF SEQUENCES: 235  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,001  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEK30.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-434-001-117

Query Match  
Best Local Similarity 57.6%; Score 14.4; DB 2; Length 70;  
Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGGCCCCCTAATA 25  
DB 60 AATAAGGCGCTCGAGCTTAACA 37

RESULT 6  
US-08-433-585-117/c

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Sequence 117, Application US/08433585
Patent No. 5763566
GENERAL INFORMATION:
APPLICANT: JENSEN, KIRK
APPLICANT: CHEN, HANG
APPLICANT: MORRIS, KEVIN
APPLICANT: MORRIS, ANDREW
APPLICANT: STEPHENS, ANDREW
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
NUMBER OF SEQUENCES: 235
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,585
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
* PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX30.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-433-585-117

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1  TITLE OF INVENTION:  SELEX
2  NUMBER OF SEQUENCES:  235
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Swanson & Bratschun, L.L.C.
5  STREET:  8400 E. Prentice Avenue, Suite 200
6  CITY:  Englewood
7  STATE:  Colorado
8  COUNTRY:  USA
9  ZIP:  80111
10
11  COMPUTER READABLE FORM:
12  MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
13  COMPUTER:  IBM pc compatible
14  OPERATING SYSTEM:  MS-DOS
15  SOFTWARE:  Wordperfect 5.1
16  CURRENT APPLICATION DATA:
17  APPLICATION NUMBER:  US/08/434,425
18  FILING DATE:
19  CLASSIFICATION:  536
20  PRIOR APPLICATION DATA:
21  APPLICATION NUMBER:  07/714,131
22  FILING DATE:  10-JUNE-1991
23  PRIOR APPLICATION DATA:
24  APPLICATION NUMBER:  07/536,428
25  FILING DATE:  11-JUNE-1990
26  PRIOR APPLICATION DATA:
27  APPLICATION NUMBER:  07/964,624
28  FILING DATE:  21-OCTOBER-1992
29  ATTORNEY/AGENT INFORMATION:
30  NAME:  Barry J. Swanson
31  REGISTRATION NUMBER:  33,215
32  REFERENCE/DOCKET NUMBER:  NEX30.1
33  TELECOMMUNICATION INFORMATION:
34  TELEPHONE:  (303) 793-3333
35  TELEFAX:  (303) 793-3433
36  INFORMATION FOR SEQ ID NO:  117:
37  SEQUENCE CHARACTERISTICS:
38  LENGTH:  70 base pairs
39  TYPE:  nucleic acid
40  STRANDEDNESS:  single
41  TOPOLOGY:  linear
42  US-08-434-425-117
43
44  Query Match      57.6%; Score 14.4; DB 2; Length 70;
45  Best Local Similarity 75.0%; Pred. No. 7.3e+02;
46  Matches  18; Conservative  0; Mismatches  6; Indels  0; Gaps  0;
47
48  Oy      2  ATTAAGGGAGCTGGAGCCCTTAATA 25
49      | | | | | | | | | | | | | | | |
50  Db      60  AATAGCGGCGCTGGAGCTTAAACA 37
51
52  RESULT 8
53  US-08-437-667-117/C
54  Sequence 117, Application US/08437667
55  Patent No. 5864026
56  GENERAL INFORMATION:
57  APPLICANT:  JENSEN, KIRK
58  APPLICANT:  CHEN, HANG
59  APPLICANT:  MORRIS, KEVIN
60  APPLICANT:  STEPHENS, ANDREW
61  APPLICANT:  GOLD, LARRY
62  TITLE OF INVENTION:  SYSTEMATIC EVOLUTION OF LIGANDS BY
63  TITLE OF INVENTION:  EXPONENTIAL ENRICHMENT;  TISSUE
64  TITLE OF INVENTION:  SELEX
65  NUMBER OF SEQUENCES:  235
66  CORRESPONDENCE ADDRESS:
67  ADDRESSEE:  Swanson & Bratschun, L.L.C.
68  STREET:  8400 E. Prentice Avenue, Suite 200
69  CITY:  Englewood
70  STATE:  Colorado
71  COUNTRY:  USA
72  ZIP:  80111
73
74  COMPUTER READABLE FORM:

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MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,667  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX30.2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ. ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-437-667-117

Query Match 57.6%; Score 14.4; DB 2; Length 70;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGGCCCTTAATA 25  
DB 60 AATAAGGGGCTGGAGCTTTAACA 37

RESULT 9  
US-08-906-955-117/c  
Sequence 117, Application US/08906955  
Patent No. 6013443  
GENERAL INFORMATION:  
APPLICANT: HEILIG, JOSEPH S.  
APPLICANT: GOLD, LARRY  
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE  
TITLE OF INVENTION: SELEX  
NUMBER OF SEQUENCES: 240  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,955  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,001

FILING DATE: 05-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX30-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ. ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-906-955-117

Query Match 57.6%; Score 14.4; DB 3; Length 70;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGGCCCTTAATA 25  
DB 60 AATAAGGGGCTGGAGCTTTAACA 37

RESULT 10  
US-08-945-909-117/c  
Sequence 117, Application US/08945909  
Patent No. 6114120  
GENERAL INFORMATION:  
APPLICANT: JENSEN, KIRK  
APPLICANT: CHEN, HANG  
APPLICANT: MORRIS, KEVIN  
APPLICANT: STEPHENS, ANDREW  
APPLICANT: GOLD, LARRY  
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS  
TITLE OF INVENTION: ENRICHMENT: TISSUE SELEX  
NUMBER OF SEQUENCES: 240  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/945,909  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/06060  
FILING DATE: 01-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,425  
FILING DATE: 03-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/437,667  
FILING DATE: 03-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,001  
FILING DATE: 03-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/433,585  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX30C-US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-945-909-117

Query Match 57.6%; Score 14.4; DB 3; Length 70;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGGCCCTTAATA 25  
DB 60 AATAAGCGGCTGGAGCTTTAACA 37

## RESULT 11

US-09-396-002A-117/C  
Sequence 117, Application US/09396002A  
Patent No. 6376474  
GENERAL INFORMATION:  
APPLICANT: HEILIG, JOSEPH S.  
GOLD, LARRY  
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
EXPONENTIAL ENRICHMENT: TISSUE SELEX  
NUMBER OF SEQUENCES: 240  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 1745 Shea Center Drive, Suite 330  
CITY: Highlands Ranch  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80129  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/396,002A  
FILING DATE: 14-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
APPLICATION NUMBER: 08/434,001  
FILING DATE: 05-MAY-1995  
APPLICATION NUMBER: 08/906,955  
FILING DATE: 05-AUGUST-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX30-5/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 268-0066  
TELEFAX: (303) 268-0065  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 117:  
US-09-396-002A-117

Query Match 57.6%; Score 14.4; DB 3; Length 70;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGGCCCTTAATA 25  
DB 60 AATAAGCGGCTGGAGCTTTAACA 37

## RESULT 12

US-10-077-319-117/C  
Sequence 117, Application US/10077319  
Patent No. 6613526  
GENERAL INFORMATION:  
APPLICANT: HEILIG, JOSEPH S.  
GOLD, LARRY

TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
EXPONENTIAL ENRICHMENT: TISSUE SELEX  
NUMBER OF SEQUENCES: 240  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 1745 Shea Center Drive, Suite 330  
CITY: Highlands Ranch  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80129

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/077,319  
FILING DATE: 14-Feb-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/396,002  
FILING DATE: 14-Sep-1999

APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
APPLICATION NUMBER: 08/434,001  
FILING DATE: 05-MAY-1995  
APPLICATION NUMBER: 08/906,955  
FILING DATE: 05-AUGUST-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX30-5/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 268-0066  
TELEFAX: (303) 268-0065

INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 117:  
US-10-077-319-117

Query Match 57.6%; Score 14.4; DB 3; Length 70;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGGCCCTTAATA 25  
DB 60 AATAAGCGGCTGGAGCTTTAACA 37

## RESULT 13

PCT-US96-06060-117/C  
Sequence 117, Application PC/TUS9606060  
GENERAL INFORMATION:  
APPLICANT: JENSEN, KIRK  
APPLICANT: CHEN, HANG  
APPLICANT: MORRIS, KEVIN  
APPLICANT: STEPHENS, ANDREW

Query Match 57.6%; Score 14.4; DB 3; Length 70;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

APPLICANT: GOLD, LARRY  
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE  
TITLE OF INVENTION: SELEX  
NUMBER OF SEQUENCES: 240  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/06060  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,425  
FILING DATE: 05-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/437,667  
FILING DATE: 05-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,001  
FILING DATE: 05-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/433,585  
FILING DATE: 05-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX30/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US96-06060-117

Query Match 57.6%; Score 14.4; DB 6; Length 70;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGGCTGAGCTTTAATA 25  
DB 60 AATAAGGGGCTGAGCTTTAACA 37

RESULT 14  
US-09-396-1966-26177  
Sequence 26177, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack

APPLICANT: David Lockhart  
APPLICANT: Altimetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26177  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-1966-26177

Query Match 56.8%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTAAAGGGGCTGAGCCCTT 21  
DB 1 TTACGGGCTCCTGACACTT 19

RESULT 15  
US-08-171-389-405  
Sequence 405, Application US/08171389  
Patent No. 5578444  
GENERAL INFORMATION:  
APPLICANT: Edwards, Cynthia A.  
APPLICANT: Cantor, Charles R.  
APPLICANT: Andrews, Beth M.  
APPLICANT: Turin, Lisa M.  
APPLICANT: Fry, Kirk B.  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
TITLE OF INVENTION: Molecules, Compositions and Methods  
NUMBER OF SEQUENCES: 641  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,389  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,936  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/723,618  
FILING DATE: 27-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/081,070  
FILING DATE: 22-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960

```

; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human adenosine deaminase gene
US-08-171-389-405

Query Match      56.8%; Score 14.2; DB 2; Length 49;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      7 GGGGCTGGCCCTTAATA 25
        |||||
Db      10 GGGGCGCGCGCGTTAAGA 28

Search completed: February 7, 2006, 12:09:00
Job time : 136 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 12:09:14 (Search time 406 Seconds  
(without alignments)  
51.606 Million cell updates/sec

Title: US-10-613-390B-1

Perfect score: 25

Sequence: 1 tattaaggggcctggcccttaata 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 6068529 seqs, 41903697 residues 11614816

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/ECT\_NEW\_PUB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	64.0	23	US-10-310-914A-1296097	Sequence 1296097,
2	15.8	63.2	21	US-10-310-914A-621697	Sequence 621697,
3	15.4	61.6	21	US-10-310-914A-679212	Sequence 679212,
4	15.4	61.6	24	US-10-310-914A-679219	Sequence 679219,
5	15	60.0	19	US-10-310-914A-627249	Sequence 627249,
6	15	60.0	25	US-11-121-849-42167	Sequence 42167, A
7	14.8	59.2	25	US-10-310-914A-760090	Sequence 760090,
8	14.6	58.4	25	US-11-121-849-615428	Sequence 615428,
9	14.4	57.6	18	US-10-310-914A-1160660	Sequence 1160660,
10	14.4	57.6	20	US-10-310-914A-236069	Sequence 236069,
11	14.4	57.6	21	US-10-310-914A-535246	Sequence 535246,
12	14.4	57.6	21	US-10-310-914A-535269	Sequence 535269,
13	14.4	57.6	23	US-10-310-914A-1296097	Sequence 1296097,
14	14.4	57.6	26	US-10-310-914A-1153244	Sequence 1153244,
15	14.2	56.8	19	US-11-101-244-1315095	Sequence 1315095,
16	14.2	56.8	19	US-11-083-784-1315095	Sequence 1315095,
17	14.2	56.8	22	US-10-310-914A-621697	Sequence 621697,
18	14.2	56.8	22	US-10-310-914A-1192905	Sequence 1192905,
19	14.2	56.8	25	US-11-121-849-518737	Sequence 518737,
20	14.2	56.8	25	US-11-121-849-518738	Sequence 518738,
21	13.8	55.2	19	US-10-310-914A-990748	Sequence 990748,
22	13.8	55.2	21	US-10-310-914A-679212	Sequence 679212,

C	23	13.8	55.2	23	7	US-10-310-914A-860902	Sequence 860902,
C	24	13.8	55.2	24	7	US-10-310-914A-679219	Sequence 679219,
C	25	13.8	55.2	25	7	US-10-310-914A-1325744	Sequence 1325744,
C	26	13.8	55.2	25	8	US-11-121-849-28266	Sequence 28266, A
C	27	13.8	55.2	25	8	US-11-121-849-38739	Sequence 38739, A
C	28	13.8	55.2	25	8	US-11-121-849-299363	Sequence 299363,
C	29	13.8	55.2	25	8	US-11-121-849-299364	Sequence 299364,
C	30	13.8	55.2	25	8	US-11-121-849-299365	Sequence 299365,
C	31	13.8	55.2	25	8	US-11-121-849-450067	Sequence 450067,
C	32	13.8	55.2	25	8	US-11-121-849-514431	Sequence 514431,
C	33	13.8	55.2	25	8	US-11-136-527-260490	Sequence 260490,
C	34	13.8	55.2	25	8	US-11-136-527-260502	Sequence 260502,
C	35	13.8	55.2	25	8	US-11-136-527-299906	Sequence 299906,
C	36	13.6	54.4	20	7	US-10-310-914A-915730	Sequence 915730,
C	37	13.6	54.4	21	7	US-10-310-914A-1053611	Sequence 1053611,
C	38	13.6	54.4	22	7	US-10-310-914A-1117125	Sequence 1117125,
C	39	13.6	54.4	25	7	US-10-310-914A-95810	Sequence 95810, A
C	40	13.6	54.4	25	7	US-10-310-914A-713535	Sequence 713535,
C	41	13.6	54.4	25	8	US-11-121-849-95350	Sequence 95350, A
C	42	13.6	54.4	25	8	US-11-121-849-292815	Sequence 292815,
C	43	13.6	54.4	25	8	US-11-121-849-442329	Sequence 442329,
C	44	13.6	54.4	25	8	US-11-121-849-442330	Sequence 442330,
C	45	13.6	54.4	25	8	US-11-121-849-613025	Sequence 613025,

## ALIGNMENTS

RESULT 1  
US-10-310-914A-1296097/C  
Sequence 1296097, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kuvatz  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1296097  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1296097

Query Match  
Best Local Similarity 100.0%, Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCT 20  
|||||  
Db 23 AAGGGGCTGGCCCT 8  
|||||

RESULT 2  
US-10-310-914A-621697  
Sequence 621697, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kuvatz  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 621697  
LENGTH: 21



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; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-621697

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 7; Length 21;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCTTAA 23
DB 1 AAGAGGCTUGGCCCUCAA 19

RESULT 3
US-10-310-914A-679212/c
; Sequence 679212, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 679212
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-679212

Query Match
Best Local Similarity 61.6%; Score 15.4; DB 7; Length 21;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TAAGGGCTGGCCCTT 20
DB 21 TAAGGGCTGGCCACT 5

RESULT 4
US-10-310-914A-679219/c
; Sequence 679219, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 679219
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-679219

Query Match
Best Local Similarity 61.6%; Score 15.4; DB 7; Length 24;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TAAGGGCTGGCCCTT 20
DB 19 TAAGGGCTGGCCACT 3

RESULT 5
US-10-310-914A-627249

; Sequence 627249, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 627249
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-627249

Query Match
Best Local Similarity 60.0%; Score 15; DB 7; Length 19;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTT 20
DB 5 AGGGGCTUGGCCCTU 19

RESULT 6
US-11-121-849-42167
; Sequence 42167, Application US/1121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 42167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-42167

Query Match
Best Local Similarity 60.0%; Score 15; DB 8; Length 25;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TATTAAGGGGCTGGCCCTTAA 23
DB 1 TATTAAGGGGCTGGCCCTTAA 23

RESULT 7
US-10-310-914A-760090/c
; Sequence 760090, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 760090
; LENGTH: 25
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TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-760090

## Query Match

Best Local Similarity 59.2%; Score 14.8; DB 7; Length 25;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAATA 23  
|||||  
Db 22 AGGGGCTGGCCCTCA 5

## RESULT 8

US-11-121-849-615428/c  
; Sequence 615428, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 615428  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-615428

## Query Match

Best Local Similarity 58.4%; Score 14.6; DB 8; Length 25;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCTTAATA 25  
|||||  
Db 25 ACGGTGCTGGCCCTTATTA 5

## RESULT 9

US-10-310-914A-1160660  
; Sequence 1160660, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1160660  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1160660

## Query Match

Best Local Similarity 57.6%; Score 14.4; DB 7; Length 18;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCCTGGCCCTTAATA 25  
|||||  
Db 2 GCCTGGCCCTCAUA 17

RESULT 10

US-10-310-914A-236069/c  
; Sequence 236069, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 236069  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-236069

## Query Match

Best Local Similarity 57.6%; Score 14.4; DB 7; Length 20;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCCTGGCCCTTAATA 25  
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Db 16 GCCTGGCCCTTAACA 1

## RESULT 11

US-10-310-914A-535246  
; Sequence 535246, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 535246  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-535246

## Query Match

Best Local Similarity 57.6%; Score 14.4; DB 7; Length 21;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCT 20  
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Db 4 AAGAGGCTGGCCCT 19

## RESULT 12

US-10-310-914A-535269  
; Sequence 535269, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 535269  
; LENGTH: 21

TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-535269

Query Match 57.6%; Score 14.4; DB 7; Length 21;  
Best Local Similarity 81.2%; Pred. No. 8.1e+02;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCT 20  
DB 6 AAGAGGCCUGGCCCU 21

RESULT 13  
US-10-310-914A-1296097  
Sequence 1296097, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kivazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1296097  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1296097

Query Match 57.6%; Score 14.4; DB 7; Length 23;  
Best Local Similarity 81.2%; Pred. No. 8.2e+02;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AAGGGGCTGGCCCTT 21  
DB 8 AAGGGGCCAGGCCCU 23

RESULT 14  
US-10-310-914A-1153244/C  
Sequence 1153244, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kivazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1153244  
LENGTH: 26  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1153244

Query Match 57.6%; Score 14.4; DB 7; Length 26;  
Best Local Similarity 93.8%; Pred. No. 8.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATTAGGGGCTGGC 16  
DB 21 TATTAGGGGCTGGC 6

RESULT 15  
US-11-101-244-1315095

Sequence 1315095, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Pharmacia, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
TITLE OF INVENTION: Scaringe, Stephen.  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1315095  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-1315095

Query Match 56.8%; Score 14.2; DB 9; Length 19;  
Best Local Similarity 63.2%; Pred. No. 1e+03;  
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 GGGGCTGGCCCTTATA 25  
DB 1 GGAGCCUGGCCUCUGAUA 19

Search completed: February 7, 2006, 12:29:26  
Job time : 406 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 10:50:27 ; Search time 1992 Seconds  
(without alignments)  
713.397 Million cell updates/sec

Title: US-10-613-390b-1

Perfect score: 25

Sequence: 1 tatcaaggagcctggcccttata 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2525446

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb\_ba:\*  
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3: gb\_env:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sce:\*  
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15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	63.2	51	6	CQ004908 Sequence
2	15.4	61.6	50	6	CQ006075 Sequence
3	15.4	61.6	50	6	CQ006077 Sequence
4	14.4	57.6	70	6	AR012502 Sequence
5	14.4	57.6	70	6	AR020330 Sequence
6	14.4	57.6	70	6	AR109351 Sequence
7	14.4	57.6	70	6	182676 Sequence 11
8	14.4	57.6	70	6	AR368542 Sequence
9	14.4	57.6	70	6	AR391734 Sequence
10	14.4	57.6	74	5	AY266911 Gadus mor
11	14.4	57.6	74	5	AY266914 Gadus mor
12	14.4	57.6	74	5	AY266915 Gadus mor
13	14.4	57.6	74	5	AY266916 Gadus mor
14	14.4	57.6	74	5	AY266917 Gadus mor
15	14.4	57.6	74	5	AY266918 Gadus mor
16	14.4	57.6	74	5	AY266920 Gadus mor
17	14.4	57.6	74	5	AY266922 Gadus mor
18	14.4	57.6	74	5	AY266925 Gadus mor

C 19	14.4	57.6	74	5	AY266926 Gadus mor
C 20	14.4	57.6	74	5	AY266927 Gadus mor
C 21	14.4	57.6	74	5	AY266930 Gadus mor
C 22	14.4	57.6	74	5	AY266932 Gadus mor
C 23	14.4	57.6	74	5	AY266939 Gadus mor
C 24	14.4	57.6	74	5	AY266944 Gadus mor
C 25	14.4	57.6	74	5	AY266949 Gadus mor
C 26	14.4	57.6	74	5	AY266951 Gadus mor
C 27	14.4	57.6	74	5	AY266952 Gadus mor
C 28	14.4	57.6	74	5	AY266954 Gadus mor
C 29	14.4	57.6	74	5	AY266956 Gadus mor
C 30	14.4	57.6	74	5	AY266964 Gadus mor
C 31	14.4	57.6	74	5	AY266966 Gadus mor
C 32	14.4	57.6	74	5	AY266967 Gadus mor
C 33	14.4	57.6	74	5	AY266968 Gadus mor
C 34	14.4	57.6	74	5	AY266973 Gadus mor
C 35	14.4	57.6	74	5	AY266974 Gadus mor
C 36	14.4	57.6	74	5	AY266975 Gadus mor
C 37	14.4	57.6	74	5	AY266980 Gadus mor
C 38	14.2	56.8	31	6	BD002349 Gene comp
C 39	14.2	56.8	49	6	AR032793 Sequence
C 40	14.2	56.8	49	6	AR032793 Sequence
C 41	14.2	56.8	49	6	129533 Sequence 40
C 42	14.2	56.8	49	6	129533 Sequence 40
C 43	14.2	56.8	49	6	191207 Sequence 40
C 44	14.2	56.8	49	6	191207 Sequence 40
C 45	14.2	56.8	49	6	AR209457 Sequence

#### ALIGNMENTS

RESULT 1	CQ004908/c	CQ004908	Sequence 3548 from Patent WO0147944.	51 bp	DNA	linear	PAT 16-JAN-2004
LOCUS	CQ004908	CQ004908					
DEFINITION	CQ004908	CQ004908					
ACCESSION	CQ004908.1	GI:41011540					
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
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Best Local Similarity							
Matches							
QY							
Db							
RESULT 2							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Carchinhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Shimkete, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0147944-A 4715 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1..50  
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/mol\_type="unassigned DNA"  
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misc\_feature 25..26  
/note="Nucleotide deleted between bases 25 and 26  
Accession number CG43256169"

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Best Local Similarity 94.1%; Pred. No. 4.5e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TAAAGGGCCTGGCCCT 20  
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44 TAAAGGGCCTGGCCACT 28

Db 44 TAAAGGGCCTGGCCACT 28

RESULT 3  
LOCUS CQ006077 50 bp DNA PAT 16-JAN-2004  
DEFINITION Sequence 4717 from Patent WO0147944.  
ACCESSION CQ006077  
VERSION CQ006077.1 GI:41012709  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Carchinhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Shimkete, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0147944-A 4717 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1..50  
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Accession number CG43256169"

ORIGIN  
Query Match 61.6%; Score 15.4; DB 6; Length 50;  
Best Local Similarity 94.1%; Pred. No. 4.5e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TAAAGGGCCTGGCCCT 20  
|||||  
18 TAAAGGGCCTGGCCACT 2

Db 18 TAAAGGGCCTGGCCACT 2

RESULT 4  
LOCUS ARO12502 70 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 117 from patent US 5763566.  
ACCESSION ARO12502

VERSION ARO12502.1 GI:3970492  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 70)  
AUTHORS Jensen, K.B., Chen, H., Morris, K.N., Stephens, A. and Gold, L.  
TITLE Systematic evolution of ligands by exponential enrichment: tissue  
JOURNAL Patent: US 5763566-A 117 09-JUN-1998;  
SELECT Location/Qualifiers  
source 1..70  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 57.6%; Score 14.4; DB 6; Length 70;  
Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGCCTGGCCCTTAATA 25  
|||||  
60 AATAAGCGGCTGGAGCTTAACA 37

Db 60 AATAAGCGGCTGGAGCTTAACA 37

RESULT 5  
LOCUS ARO20330 70 bp DNA PAT 05-DEC-1998  
DEFINITION Sequence 117 from patent US 5789157.  
ACCESSION ARO20330  
VERSION ARO20330.1 GI:3974945  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 70)  
AUTHORS Jensen, K.B., Chen, H., Morris, K.N., Stephens, A. and Gold, L.  
TITLE Systematic evolution of ligands by exponential enrichment: tissue  
JOURNAL Patent: US 5789157-A 117 04-AUG-1998;  
SELECT Location/Qualifiers  
source 1..70  
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ORIGIN  
Query Match 57.6%; Score 14.4; DB 6; Length 70;  
Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGCCTGGCCCTTAATA 25  
|||||  
60 AATAAGCGGCTGGAGCTTAACA 37

Db 60 AATAAGCGGCTGGAGCTTAACA 37

RESULT 6  
LOCUS ARO109351 70 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 117 from patent US 6114120.  
ACCESSION ARO109351  
VERSION ARO109351.1 GI:12825627  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 70)  
AUTHORS Jensen, K.B., Chen, H., Morris, K.N., Stephens, A. and Gold, L.  
TITLE Systematic evolution of ligands by exponential enrichment: tissue  
JOURNAL Patent: US 6114120-A 117 05-SEP-2000;  
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ORIGIN /mol\_type="unassigned DNA"

Query Match 57.6%; Score 14.4; DB 6; Length 70;  
Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGCGCTGAGCTTTAACA 25  
DB 60 AATAGCGGCTTGAGCTTTAACA 37

RESULT 7  
LOCUS 182676 70 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 117 from patent US 5712375.  
ACCESSION 182676  
VERSION 182676.1 GI:3210973  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 70)  
AUTHORS Jensen,K.B., Chen,H., Morris,K.N., Stephens,A. and Gold,L.  
TITLE Systematic evolution of ligands by exponential enrichment: tissue  
select

JOURNAL Patent: US 5712375-A 117 27-JAN-1998;  
FEATURES Location/Qualifiers

ORIGIN 1.70  
/organism="unknown"  
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Query Match 57.6%; Score 14.4; DB 6; Length 70;  
Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGCGCTGAGCTTTAACA 25  
DB 60 AATAGCGGCTTGAGCTTTAACA 37

RESULT 8  
LOCUS AR368542 70 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 117 from patent US 6376474.  
ACCESSION AR368542  
VERSION AR368542.1 GI:34602693  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 70)  
AUTHORS Heilig,J.S. and Gold,L.  
TITLE Systematic evolution of ligands by exponential enrichment: tissue  
select

JOURNAL Patent: US 6376474-A 117 23-APR-2002;  
FEATURES Location/Qualifiers

ORIGIN 1.70  
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Query Match 57.6%; Score 14.4; DB 6; Length 70;  
Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGCGCTGAGCTTTAACA 25  
DB 60 AATAGCGGCTTGAGCTTTAACA 37

RESULT 9  
LOCUS AR391734 70 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 117 from patent US 6613526.  
ACCESSION AR391734  
VERSION AR391734.1 GI:40115328  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 70)  
AUTHORS Heilig,J.S. and Gold,L.  
TITLE Systematic evolution of ligands by exponential enrichment: tissue  
select

JOURNAL Patent: US 6613526-A 117 02-SEP-2003;  
FEATURES Location/Qualifiers

ORIGIN 1.70  
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Query Match 57.6%; Score 14.4; DB 6; Length 70;  
Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATTAAGGGCGCTGAGCTTTAACA 25  
DB 60 AATAGCGGCTTGAGCTTTAACA 37

RESULT 10  
LOCUS AY266911 74 bp DNA linear VRT 16-DEC-2003  
DEFINITION Gadsu morhua isolate TFA7.04 haplotype S02 mitochondrial  
RNA-Thr-tRNA-Pro intergenic spacer, complete sequence.

ACCESSION AY266911  
VERSION AY266911.1 GI:33089797  
KEYWORDS  
SOURCE  
ORGANISM

mitochondrion Gadsu morhua (Atlantic cod)  
Gadsu morhua

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadsu.

1 (bases 1 to 74)

REFERENCE 1 (bases 1 to 74)  
AUTHORS Sigurgislaason,H. and Arnason,E.  
TITLE Extent of mitochondrial DNA sequence variation in Atlantic cod from  
the Faroe Islands: a resolution of gene genealogy

JOURNAL Heredity 91 (6), 557-564 (2003)  
REFERENCE PUBMED 14560303

2 (bases 1 to 74)  
AUTHORS Sigurgislaason,H. and Arnason,E.  
TITLE Direct Substitution

JOURNAL Submitted (01-APR-2003) Institute of Biology, University of  
Iceland, Grenasavegur 12, Reykjavik IS-108, Iceland

FEATURES Location/Qualifiers

ORIGIN 1.74  
/organism="Gadsu morhua"  
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/db\_xref="taxon:8049"  
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/country="Faroe Islands"  
/note="cRNA-Thr-tRNA-Pro intergenic spacer"

Query Match 57.6%; Score 14.4; DB 5; Length 74;  
Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY      2 ATTAAGGGCGCTGGCCCTTAATA 25
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Db      33 ATTATGGGGCGCTCCCGGTAATA 10

RESULT 11
AY266914/c      74 bp DNA linear VRT 16-DEC-2003
LOCUS      Gadus morhua isolate TFA7.07 haplotype S06 mitochondrial
DEFINITION rRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION      AY266914
VERSION
KEYWORDS
SOURCE
ORGANISM      mitochondrion Gadus morhua (Atlantic cod)
      Gadus morhua
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
      Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE
AUTHORS      Sigurgislaeson,H. and Arnason,E.
TITLES      Extent of mitochondrial DNA sequence variation in Atlantic cod from
      the Faroe Islands: a resolution of gene genealogy
JOURNAL      Hereditas 91 (6), 557-564 (2003)
PUBMED      14560303
REFERENCE
AUTHORS      Sigurgislaeson,H. and Arnason,E.
TITLES      Direct Submission
      Submitted (01-APR-2003) Institute of Biology, University of
      Iceland, Grensavesgur 12, Reykjavik IS-108, Iceland
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ORIGIN
Query Match      57.6%; Score 14.4; DB 5; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY      2 ATTAAGGGCGCTGGCCCTTAAT 25
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Db      33 ATTATGGGGCGCTCTCCCGTAATA 10

RESULT 12
AY266915/c      74 bp DNA linear VRT 16-DEC-2003
LOCUS      Gadus morhua isolate TFA7.08 haplotype S06 mitochondrial
DEFINITION rRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION      AY266915
VERSION
KEYWORDS
SOURCE
ORGANISM      mitochondrion Gadus morhua (Atlantic cod)
      Gadus morhua
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
      Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE
AUTHORS      Sigurgislaeson,H. and Arnason,E.
TITLES      Extent of mitochondrial DNA sequence variation in Atlantic cod from
      the Faroe Islands: a resolution of gene genealogy
JOURNAL      Hereditas 91 (6), 557-564 (2003)
PUBMED      14560303
REFERENCE
AUTHORS      Sigurgislaeson,H. and Arnason,E.
TITLES      Direct Submission
      Submitted (01-APR-2003) Institute of Biology, University of
      Iceland, Grensavesgur 12, Reykjavik IS-108, Iceland
FEATURES
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ORIGIN
Query Match      57.6%; Score 14.4; DB 5; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY      2 ATTAAGGGCGCTGGCCCTTAATA 25
      ||||| ||||| ||||| |||||
Db      33 ATTATGGGGCGCTCTCCCGTAATA 10

```

```

AUTHORS      Sigurgislaeson,H. and Arnason,E.
TITLES      Direct Submission
JOURNAL      Submitted (01-APR-2003) Institute of Biology, University of
      Iceland, Grensavesgur 12, Reykjavik IS-108, Iceland
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      1..74
      /note="tRNA-Thr-tRNA-Pro intergenic spacer"

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Query Match      57.6%; Score 14.4; DB 5; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY      2 ATTAAGGGCGCTGGCCCTTAATA 25
      ||||| ||||| ||||| |||||
Db      33 ATTATGGGGCGCTCTCCCGTAATA 10

RESULT 13
AY266916/c      74 bp DNA linear VRT 16-DEC-2003
LOCUS      Gadus morhua isolate TFA7.09 haplotype S06 mitochondrial
DEFINITION rRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION      AY266916
VERSION
KEYWORDS
SOURCE
ORGANISM      mitochondrion Gadus morhua (Atlantic cod)
      Gadus morhua
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
      Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE
AUTHORS      Sigurgislaeson,H. and Arnason,E.
TITLES      Extent of mitochondrial DNA sequence variation in Atlantic cod from
      the Faroe Islands: a resolution of gene genealogy
JOURNAL      Hereditas 91 (6), 557-564 (2003)
PUBMED      14560303
REFERENCE
AUTHORS      Sigurgislaeson,H. and Arnason,E.
TITLES      Direct Submission
      Submitted (01-APR-2003) Institute of Biology, University of
      Iceland, Grensavesgur 12, Reykjavik IS-108, Iceland
FEATURES
      source
      1..74
      /organism="Gadus morhua"
      /organelle="mitochondrion"
      /mol_type="genomic DNA"
      /isolate="TFA7.09"
      /isolation_source="Station A"
      /db_xref="taxon:8049"
      /haplotype="S06"
      /country="Faroe Islands"
      1..74
      /note="tRNA-Thr-tRNA-Pro intergenic spacer"

ORIGIN
Query Match      57.6%; Score 14.4; DB 5; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY      2 ATTAAGGGCGCTGGCCCTTAATA 25
      ||||| ||||| ||||| |||||
Db      33 ATTATGGGGCGCTCTCCCGTAATA 10

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RESULT 14
AY266917/c 74 bp DNA linear VRT 16-DEC-2003
LOCUS
DEFINITION
Gadus morhua isolate TFA7.10 haplotype S03 mitochondrial
cRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION
AY266917
VERSION
AY266917.1 GI:33089803
KEYWORDS
SOURCE
ORGANISM
mitochondrion Gadus morhua (Atlantic cod)
Gadus morhua
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE
AUTHORS
1 (bases 1 to 74)
Sjurgislaason, H. and Arnason, E.
TITLE
Extent of mitochondrial DNA sequence variation in Atlantic cod from
the Faroe Islands: a resolution of gene genealogy
JOURNAL
Heredity 91 (6), 557-564 (2003)
PUBMED
14560303
2 (bases 1 to 74)
Sjurgislaason, H. and Arnason, E.
REFERENCE
Direct Submission
AUTHORS
Submitted (01-APR-2003) Institute of Biology, University of
Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
LOCATION/Qualifiers
1. .74
/organism="Gadus morhua"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="TFA7.10"
/isolation source="Station A"
/db_xref="taxon:8049"
/haplotype="S03"
/country="Faroe Islands"
1. .74
/note="cRNA-Thr-tRNA-Pro intergenic spacer"

ORIGIN
misc_feature

Query Match 57.6%; Score 14.4; DB 5; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATTAAGGGGCGCTGCGCCCTTAATA 25
||||| ||| ||| |||
Db 33 ATTATGGGGCGTCTCCCGTAATA 10

RESULT 15
AY266918/c 74 bp DNA linear VRT 16-DEC-2003
LOCUS
DEFINITION
Gadus morhua isolate TFA7.11 haplotype S06 mitochondrial
cRNA-Thr-tRNA-Pro intergenic spacer, complete sequence.
ACCESSION
AY266918
VERSION
AY266918.1 GI:33089804
KEYWORDS
SOURCE
ORGANISM
mitochondrion Gadus morhua (Atlantic cod)
Gadus morhua
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE
AUTHORS
1 (bases 1 to 74)
Sjurgislaason, H. and Arnason, E.
TITLE
Extent of mitochondrial DNA sequence variation in Atlantic cod from
the Faroe Islands: a resolution of gene genealogy
JOURNAL
Heredity 91 (6), 557-564 (2003)
PUBMED
14560303
2 (bases 1 to 74)
Sjurgislaason, H. and Arnason, E.
REFERENCE
Direct Submission
AUTHORS
Submitted (01-APR-2003) Institute of Biology, University of
Iceland, Grensasvegur 12, Reykjavik IS-108, Iceland
LOCATION/Qualifiers

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source
1. .74
/organism="Gadus morhua"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="TFA7.11"
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/haplotype="S06"
/country="Faroe Islands"
1. .74
/note="cRNA-Thr-tRNA-Pro intergenic spacer"

ORIGIN
misc_feature

Query Match 57.6%; Score 14.4; DB 5; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATTAAGGGGCGCTGCGCCCTTAATA 25
||||| ||| ||| |||
Db 33 ATTATGGGGCGTCTCCCGTAATA 10

Search completed: February 8, 2006, 03:43:16
Job time: 1993 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 12:06:52 ; Search time 794 Seconds

(without alignments)  
260.371 Million cell updates/sec

Title: US-10-613-390B-1

Perfect score: 25

Sequence: 1 tattaaggagcctgcgccttaata 25

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 11330536

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	7	US-10-613-390B-1
2	23.4	93.6	25	7	US-10-613-390B-1
3	17.4	69.6	25	9	US-10-809-189-116728
4	15.8	63.2	25	8	US-10-719-900-27015
5	15.8	63.2	25	8	US-10-719-900-27016
6	15.8	63.2	25	9	US-10-809-189-116728
7	15.8	63.2	25	10	US-11-036-317-189638
8	15.8	63.2	25	10	US-11-036-317-226389
9	15.8	63.2	25	10	US-11-036-317-273256
10	15.8	63.2	25	10	US-11-036-317-295882
11	15.8	63.2	25	10	US-11-036-317-303549
12	15.8	63.2	25	10	US-11-036-317-374272
13	15.8	63.2	25	10	US-11-036-317-739211
14	15.4	61.6	25	10	US-11-060-756-172272
15	15.2	60.8	25	7	US-10-719-956-370902
16	15.2	60.8	25	8	US-10-719-956-370902
17	14.8	59.2	25	9	US-10-809-189-86335
18	14.8	59.2	25	9	US-10-809-189-86336
19	14.8	59.2	25	10	US-11-036-317-451864
20	14.6	58.4	25	7	US-10-719-956-567778
21	14.6	58.4	25	7	US-10-719-956-567779
22	14.4	57.6	25	10	US-11-036-317-208481
23	14.4	57.6	25	10	US-11-036-317-249444

24	14.4	57.6	25	10	US-11-036-317-263488	Sequence 263488,
25	14.4	57.6	25	10	US-11-036-317-298920	Sequence 298920,
26	14.4	57.6	25	10	US-11-036-317-343406	Sequence 343406,
27	14.4	57.6	25	10	US-11-036-317-361767	Sequence 361767,
28	14.4	57.6	25	10	US-11-060-756-134392	Sequence 134392,
29	14.4	57.6	25	10	US-11-060-756-297112	Sequence 297112,
30	14.4	57.6	70	5	US-10-077-319-117	Sequence 117, App
31	14.2	56.8	25	7	US-10-719-956-305034	Sequence 305034,
32	14.2	56.8	25	8	US-10-719-900-27015	Sequence 27015, A
33	14.2	56.8	25	8	US-10-719-900-255528	Sequence 255528,
34	14.2	56.8	25	8	US-10-719-900-255528	Sequence 255528,
35	14.2	56.8	25	8	US-10-719-900-800772	Sequence 800772,
36	14.2	56.8	25	9	US-10-809-189-26177	Sequence 26177, A
37	14.2	56.8	25	9	US-10-809-189-26177	Sequence 26177, A
38	14.2	56.8	25	10	US-11-036-317-189638	Sequence 189638,
39	14.2	56.8	25	10	US-11-036-317-226389	Sequence 226389,
40	14.2	56.8	25	10	US-11-036-317-273256	Sequence 273256,
41	14.2	56.8	25	10	US-11-036-317-295882	Sequence 295882,
42	14.2	56.8	25	10	US-11-036-317-303549	Sequence 303549,
43	14.2	56.8	25	10	US-11-036-317-374272	Sequence 374272,
44	14.2	56.8	25	10	US-11-036-317-739211	Sequence 739211,
45	14.2	56.8	25	10	US-11-036-317-739212	Sequence 739212,

## ALIGNMENTS

RESULT 1  
US-10-613-390B-1  
; Sequence 1, Application US/10613390B  
; Publication No. US20040127442A1  
; GENERAL INFORMATION:  
; APPLICANT: Gene Cloning Inc  
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders  
; FILE REFERENCE: 60/400,137  
; CURRENT APPLICATION NUMBER: US/10/613,390B  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 10/613390  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic primer  
US-10-613-390B-1

Query Match 100.0%; Score 25; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTAAAGGAGCTGCGCCCTTAATA 25  
Db 1 TATTAAAGGAGCTGCGCCCTTAATA 25

RESULT 2  
US-10-613-390B-1/c  
; Sequence 1, Application US/10613390B  
; Publication No. US20040127442A1  
; GENERAL INFORMATION:  
; APPLICANT: Gene Cloning Inc  
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders  
; FILE REFERENCE: 60/400,137  
; CURRENT APPLICATION NUMBER: US/10/613,390B  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 10/613390  
; PRIOR FILING DATE: 2003-07-03  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1

LENGTH: 25  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic primer  
US-10-613-390b-1

Query Match 93.6%; Score 23.4; DB 7; Length 25;  
Best Local Similarity 96.0%; Pred. No. 0.3;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATTAAGGCGCTGGCCCTTAATA 25  
DB 25 TATTAAGGCGCGAGCCCTTAATA 1

## RESULT 3

US-10-809-189-116728/c  
Sequence 116728, Application US/10809189  
Publication No. US20050048531A1  
GENERAL INFORMATION:

APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 116728

LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-10-809-189-116728

Query Match 69.6%; Score 17.4; DB 9; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24  
DB 25 AGGGGCTGGCCCTTAAT 7

## RESULT 4

US-10-719-900-27015/c  
Sequence 27015, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
APPLICANT: David Lockhart  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 27015  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-27015

Query Match 63.2%; Score 15.8; DB 8; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24  
DB 24 AGGGGCTGGCCCTTAAT 6

## RESULT 5

US-10-719-900-27016/c  
Sequence 27016, Application US/10719900  
Publication No. US20050026164A1  
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
APPLICANT: David Lockhart  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 27016  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-27016

Query Match 63.2%; Score 15.8; DB 8; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24  
DB 24 AGGGGCTGGCCCTTAAT 6

## RESULT 6

US-10-809-189-116728  
Sequence 116728, Application US/10809189  
Publication No. US20050048531A1  
GENERAL INFORMATION:

APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 116728  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-10-809-189-116728

Query Match 63.2%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATTAAGGCGCTGGCCCTT 20  
DB 7 ATTAAGGCGCGAGCCCTT 25

## RESULT 7

US-11-036-317-189638  
Sequence 189638, Application US/11036317  
Publication No. US20050214823A1

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/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 189638
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-189638

Query Match          63.2%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24
DB 3 AGAGGCTG3CCCCCTTCAT 21

RESULT 8
US-11-036-317-226389
/ Sequence 226389, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 226389
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-226389

Query Match          63.2%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24
DB 4 AGAGGCTG3CCCCCTTCAT 22

RESULT 9
US-11-036-317-273256
/ Sequence 273256, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 273256
/ LENGTH: 25

/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-273256

Query Match          63.2%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24
DB 5 AGAGGCTG3CCCCCTTCAT 23

RESULT 10
US-11-036-317-295882
/ Sequence 295882, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 295882
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-295882

Query Match          63.2%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24
DB 2 AGAGGCTG3CCCCCTTCAT 20

RESULT 11
US-11-036-317-303549
/ Sequence 303549, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 303549
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-303549

Query Match          63.2%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAAT 24
DB 5 AGAGGCTG3CCCCCTTCAT 23
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RESULT 12  
US-11-036-317-374272  
; Sequence 374272, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 374272  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-374272

Query Match 63.2%; Score 15.8; DB 10; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTAT 24  
DB 6 AGAGGCTGGCCCTTCAT 24

RESULT 13  
US-11-036-317-739211/c  
; Sequence 739211, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 739211  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-739211

Query Match 63.2%; Score 15.8; DB 10; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTAGGGGCTGGCCCTTA 22  
DB 19 TTAGGGGCTGGCCACTTA 1

RESULT 14  
US-11-060-756-172272/c  
; Sequence 172272, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 172272  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-172272

Query Match 61.6%; Score 15.4; DB 10; Length 25;  
Best Local Similarity 94.1%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGGGGCTGGCCCTTA 22  
DB 25 AGGGGCTGGCCCATTA 9

RESULT 15  
US-10-719-956-370902  
; Sequence 370902, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 370902  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-370902

Query Match 60.8%; Score 15.2; DB 7; Length 25;  
Best Local Similarity 85.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTAGGGGCTGGCCCTTA 22  
DB 4 TTAGGGGCTGGCCCTTA 23

Search completed: February 7, 2006, 12:22:29  
Job time : 795 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 11:01:48 ; Search time 3599 Seconds  
(without alignments)

325.001 Million cell updates/sec

Title: US-10-613-390b-1

Sequence: 1 tattaaggagcctggcccttaata 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 778150

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_esc4:\*  
5: gb\_esc5:\*  
6: gb\_esc6:\*  
7: gb\_esc7:\*  
8: gb\_esc8:\*  
9: gb\_esc9:\*  
10: gb\_esc10:\*  
11: gb\_esc11:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	16	64.0	83	5	BU812825
2	15.8	63.2	78	1	AM250424
3	15.4	61.6	40	9	AZ371110
4	15.4	61.6	40	9	AZ371110
5	15.4	61.6	83	9	AZ440331
6	15.2	60.8	98	1	AM770417
7	15	60.0	64	1	AI149654
8	15	60.0	70	10	CG527767
9	15	60.0	73	1	AM251001
10	15	60.0	86	10	CG524805
11	15	60.0	94	7	CK428180
12	14.6	58.4	53	10	CR169973
13	14.6	58.4	61	11	CR169973
14	14.6	58.4	64	10	CG650062
15	14.6	58.4	64	10	CG650062
16	14.4	57.6	42	10	CG650062
17	14.4	57.6	83	5	BU812825
18	14.4	57.6	84	5	CP102969
19	14.4	57.6	91	6	CF641086
20	14.2	56.8	46	10	CL529021
21	14.2	56.8	47	9	AZ651810
22	14.2	56.8	66	10	CG482226

C 23	14.2	56.8	78	1	AM250424	AM250424 2822310.3
C 24	14.2	56.8	84	10	CZ44284	CZ44284 AE0876 Sa
C 25	14.2	56.8	89	6	CB930280	CB930280 r193a05.Y
C 26	14.2	56.8	89	6	CB930280	CB930280 r193a05.Y
C 27	14.2	56.8	28	1	AA870545	AA870545 vq23a04.E
C 28	14	56.0	55	11	GG4350127	AJ582875 Gallus ga
C 29	13.8	55.2	46	1	AI582875	AI582875 Galus ga
C 30	13.8	55.2	58	10	AJ587174	AJ587174 Arabidops
C 31	13.8	55.2	70	9	AZ484117	AZ484117 IM0310N16
C 32	13.8	55.2	71	10	CM083263	CM083263 104.425.1
C 33	13.8	55.2	78	10	CG538865	CG538865 OST129261
C 34	13.8	55.2	78	10	CG680849	CG680849 89M06.40
C 35	13.8	55.2	79	1	AI686688	AI686688 tns5g10.X
C 36	13.8	55.2	83	9	AZ440331	AZ440331 IM0231A20
C 37	13.8	55.2	85	11	CR102161	CR102161 Reverse s
C 38	13.8	55.2	96	3	Bj076360	Bj076360 Bj076360
C 39	13.8	55.2	96	11	CR131012	CR131012 Reverse s
C 40	13.8	55.2	97	6	CD979428	CD979428 QNG3D11.Y
C 41	13.8	55.2	100	10	CG553173	CG553173 OST165393
C 42	13.6	54.4	50	9	AZ423820	AZ423820 IM0203P22
C 43	13.6	54.4	67	10	CG525840	CG525840 OST101409
C 44	13.6	54.4	71	1	AA452589	AA452589 zx39f02.B
C 45	13.6	54.4	76	10	CG573029	CG573029 OST204293

#### ALIGNMENTS

RESULT 1  
LOCUS BU812825 83 bp mRNA linear EST 15-OCT-2002  
DEFINITION NO01H03 Populus bark cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION BU812825.1 GI:22968143  
VERSION BU812825.1  
KEYWORDS EST.  
SOURCE Populus tremula x Populus tremuloides  
ORGANISM Populus tremula x Populus tremuloides

REFERENCE Umeberg, P., Bhalero, R.R., Jansson, S. and Sterky, P.  
1 (bases 1 to 83)

AUTHORS The Poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries

JOURNAL Unpublished (2002)

COMMENT Contact: BHALERAO RUPALI R.

Umea Plant Science Center

Department of Plant Physiology

University of Umea, 901 87 Umea, Sweden

Tel: +46 90 786 5279

Fax: +46 90 786 6676

Email: rupali.bhalerao@plantphys.umu.se

FEATURES  
source location/Qualifiers

1..83  
/organism="Populus tremula x Populus tremuloides"  
/mol\_type="mRNA"  
/db\_xref="taxon:47664"  
/tissue\_type="bark"  
/clone\_lib="Populus bark cDNA library"

#### ORIGIN

Query Match 64.0% Score 16; DB 5; Length 83;  
Best Local Similarity 79.2% Pred. 1.3e+04;  
Matches 19; Conservative 0; Mismatches 5; Indels 0;

QY 2 ATTAAGGAGGAGCTGGCCCTTATA 25  
|||||  
DB 33 ATTAAGGAGGAGCTGGCTTATA 56  
|||||

RESULT 2  
AM250424

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurgnathi; Murioidea; Muridae; Murinae; Mus. 1 (bases 1 to 40) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.: Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0122 row: I column: 05 Seq primer: CGTTGTAACAGACGCCACGT Class: plasmid ends High quality sequence stop: 40.
FEATURES	location/Qualifiers 1..40 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUCGM0122105". /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 [gil4732114[gb AF129072.1], a copy-number inducible derivative of plasmid Rt. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN	Query Match 61.6%; Score 15.4; DB 9; Length 40; Best Local Similarity 76.0%; Pred.No. 2.3e+04; Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
CY	1 TATTAAAGGGCGCTGCGCCCTTATA 25                           Db 13 TATTATGGGTAATGGCCCATTTATA 37
RESULT 4	AZ371110 40 bp DNA linear GSS 02-OCT-2000
LOCUS	JM0122105F Mouse 10kb plasmid UGCIM library Mus musculus genomic
DEFINITION	clone UUCGM0122105 F, genomic survey sequence.
ACCSSION	AZ371110

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurgnathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 40) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Relly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts unpublished (2000)
TITLE	University of Utah Genome Center University of Utah 84112, USA Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
JOURNAL	84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu
COMMENT	Insert length: 10000 Std Error: 0.00 Plate: 0122 row: I column: 05 Seq primer: CGTTGTAACAGACGCCACGT Class: plasmid ends High quality sequence stop: 40. Location/Qualifiers 1. 40 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUCGM0122105". /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 [gil4732114[gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN	
Query Match	61.6%; Score 15.4; DB 9; Length 40;
Best Local Similarity	76.0%; Pred. No. 2.3e+04;
Matches 19; Conservative	0; Mismatches 6; Indels 0; Gaps 0;
Cy	1 TATTAAAGGGCGCTGCGCCCTTATA 25                           Db 13 TATTATGGGTAATGGCCCATTTATA 37
RESULT 4	AZ371110 40 bp DNA linear GSS 02-OCT-2000
AZ371110/c	LOCUS
DEFINITION	JM012210SF Mouse 10kb plasmid UGCIM library Mus musculus genomic
clone UUCGM0122105 F,	genomic survey sequence.
ACCSSION	AZ371110

VERSION AZ271110.1 GI:10484810  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 40)  
 Duna, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0122 row: I column: 05  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 40.  
 Location/Qualifiers  
 1. 40  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U061M0122105"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U061M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
 Query Match 61.6%; Score 15.4; DB 9; Length 40;  
 Best Local Similarity 76.0%; Pred. No. 2.3e+04;  
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 1 TATTAGGGGCGCTGGCCCTTAATA 25  
 |||||  
 37 TATTATGGGCGCCATACCATATA 13

RESULT 5  
 AZ440331/c 83 bp DNA linear GSS 03-OCT-2000  
 LOCUS IM0231A20F Mouse 10kb plasmid U061M library Mus musculus genomic  
 DEFINITION clone U061M0231A20 F, genomic survey sequence.

ACCESSION AZ440331 GI:10564344  
 VERSION AZ440331.1  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 83)  
 Duna, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0231 row: A column: 20  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 83.  
 Location/Qualifiers  
 1. 83  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U061M0231A20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U061M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
 Query Match 61.6%; Score 15.4; DB 9; Length 83;  
 Best Local Similarity 94.1%; Pred. No. 2.4e+04;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 8 GGGCGCTGGCCCTTAAT 24  
 |||||  
 68 GGGCGCTGGCCCTTAAT 52

RESULT 6  
 AW770417/c 98 bp mRNA linear EST 04-MAY-2000  
 LOCUS AW770417  
 DEFINITION h18a12.x1 NCI\_CGAP\_Kid13 Homo sapiens cDNA clone IMAGE:3007582 3'

RNA sequence.

ACCESSION AM770417  
VERSION AW770417.1 GI:7702459  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo

1 (bases 1 to 98)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: [info@image.llnl.gov](mailto:info@image.llnl.gov)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 73.  
Location/Qualifiers

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3007582"  
/tissue\_type="2 pooled Wilms' tumors, one primary and one metastatic to brain"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site\_1: Salt; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. library constructed by Life Technologies."

ORIGIN

Query Match 60.8%; Score 15.2; DB 1; Length 98;  
Best Local Similarity 85.0%; Pred. No. 3.1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 AGGGGCGTGGCCCTTAATA 25  
|||  
Db 95 AGGGGCGTGGCCCGACACA 76  
|||

RESULT 7  
A1149654 64 bp mRNA linear EST 10-NOV-1998  
LOCUS af37c02.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752194  
DEFINITION 3', similar to gb:M61866 ZINC FINGER PROTEIN 85 (HUMAN);, mRNA  
sequence.  
A1149654  
A1149654.1 GI:3678123  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo

1 (bases 1 to 64)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 1082 Std Error: 0.00  
Seq primer: -40m3 fwd. Et from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1752194"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT7T3p-Pac (pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech laboratories, Inc., and primed with a Not I - oligo (dt) primer [5', TGTTACGATCGAAGTGGAGCGCGCCCGCAATTTTTTTTTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 60.0%; Score 15; DB 1; Length 64;  
Best Local Similarity 78.3%; Pred. No. 3.7e+04;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TATTAGGGGCGTGGCCCTTA 23  
|||  
Db 12 TATTAGGGGCGTGGCGCTTAA 34  
|||

RESULT 8  
CG527767/c 70 bp mRNA linear GSS 01-OCT-2003  
LOCUS OST106096 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST106096,  
DEFINITION mRNA sequence.  
CG527767  
CG527767.1 GI:37314339  
GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 70)  
Zambrowicz, B.P., Abidin, A., Ramirez-Solis, R., Richter, L.J., Pigott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W., Jr., Kipp, P., Kohhauf, B., Ma, Z.-Q., Matkovich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.  
Mnki kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
14610273  
Contact: Zambrowicz BP  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: [materials@lexgen.com](mailto:materials@lexgen.com)  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
Location/Qualifiers



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1..70
/organism="Mus musculus"
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/strain="129Sv/Ev"
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/clone="OST106096"
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ORIGIN

Query Match      60.0%; Score 15; DB 10; Length 70;
Best Local Similarity 78.3%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY
2 ATTAGGGGCTGCGCCCTTAAT 24
|||||
53 ATCATGGGCTGCTGCTCGAAT 31

RESULT 9
LOCUS      AW251001      73 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION 2821159.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821159 3',
            mRNA sequence.
ACCESSION  AW251001
VERSION     AW251001.1 GI:6593947
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
1 (bases 1 to 73)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821159.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LINL at:
www.bio.lnrl.gov/bhrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
low Quality Sequence: Trace file contained 73 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: L16M6 row: B column: 8
High quality sequence stop: 10.
Location/Qualifiers
1..73
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/clone="IMAGE:2821159"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

```

```

the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match      60.0%; Score 15; DB 1; Length 73;
Best Local Similarity 78.3%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY
3 TTATAGGGGCTGCGCCCTTAATA 25
|||||
52 TTCCGGGGGCTGCGCCCTCAATA 30

RESULT 10
LOCUS      CG524805      86 bp      mRNA      linear      GSS 01-OCT-2003
DEFINITION OST19167 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST19167,
            mRNA sequence.
ACCESSION  CG524805
VERSION     CG524805.1 GI:37311377
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 86)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J.J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materiel@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers
1..86
/organism="Mus musculus"
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/strain="129Sv/Ev"
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/clone="OST19167"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match      60.0%; Score 15; DB 10; Length 86;
Best Local Similarity 78.3%; Pred. No. 3.8e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY
1 TTATAGGGGCTGCGCCCTTAAT 23
|||||
84 TTATCCAGGGCTTGGCCCTTCA 62

RESULT 11
LOCUS      CK428180      94 bp      mRNA      linear      EST 06-JAN-2004
DEFINITION Taji1907.Y1 Gastric Epithelial Progenitor 2 Mus musculus cDNA 5',
            mRNA sequence.
ACCESSION  CK428180

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VERSION CK428180.1 GI:40672576  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 1 (bases 1 to 94)  
 REFERENCE  
 AUTHORS Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Rutter, E., Bannet, J., Ronko, I., Tsagarishevili, R., Belaygorod, L., Grow, A., Maguire, L., Waterston, R. and Wilson, R.  
 Washu Stem Cell EST Project  
 TITLE Washu Stem Cell EST Project  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Jeff Gordon and Mike Lovett  
 Washu, Human Genetics Division  
 Washington University School of Medicine  
 1st strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pAMP1 vector in annealing reaction with uracil DNA glycosylase (UDG). Library constructed by Y. Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI.  
 Putative full length read  
 vector to vector length is  
 Seq primer: -40RP from Gibco.  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 /tissue\_type="Laser-captured isthmal cells from tox176 transgenic mice"  
 /dev\_stage="adult"  
 /lab\_host="DH5alpha"  
 /note="Vector: pAMP1; 1st strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pAMP1 vector in annealing reaction with uracil DNA glycosylase (UDG). Library constructed by Y. Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI."  
 ORIGIN  
 Query Match 60.0%; Score 15; DB 7; Length 94;  
 Best Local Similarity 78.3%; Pred. No. 3.8e+04;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 TATTAGGGCGCTGGCCCTTA 23  
 Db 43 TATTCTTGGGCGTGGCCCTTA 21  
 RESULT 12  
 CL880134 53 bp DNA linear GSS 30-AUG-2004  
 LOCUS abf42c10.y1 Soybean random, unfiltered genomic library glycine max  
 DEFINITION genomic, genomic survey sequence.  
 ACCESSION CL880134  
 VERSION CL880134.1 GI:51614669  
 KEYWORDS GSS.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine  
 1 (bases 1 to 53)  
 REFERENCE  
 AUTHORS Nunberg, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J., Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H. and Stacey, G.  
 Methylation filtered genomic sequences from Glycine max

JOURNAL Unpublished (2004)  
 COMMENT Contact: Gary Stacey  
 University of Missouri  
 108 Waters Hall, Columbia, MO 65211, USA  
 Tel: 573-884-1267  
 Fax: 573-882-0588  
 Email: stacey@missouri.edu  
 LIdID: 230  
 Class: shotgun.  
 Location/Qualifiers  
 1..53  
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 ORIGIN  
 Query Match 58.4%; Score 14.6; DB 10; Length 53;  
 Best Local Similarity 81.0%; Pred. No. 5.6e+04;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TATTAGGGCGCTGGCCCTT 21  
 Db 38 TCTTAGGTGTGTGGCCCTT 18  
 RESULT 13  
 CR169973 61 bp DNA linear GSS 06-JUN-2004  
 LOCUS CR169973  
 DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN50C03, genomic survey sequence.  
 ACCESSION CR169973  
 VERSION CR169973.1 GI:49948822  
 KEYWORDS GSS; genome survey sequence; MTCR.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 1 (bases 1 to 61)  
 REFERENCE  
 AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.  
 Direct Submission  
 TITLE Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 JOURNAL CB10 ISA, UK. <http://www.sanger.ac.uk/MTCR>  
 Location/Qualifiers  
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 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 ATTAAGGGCGCTGGCCCTTA 22  
 Db 16 ATTAAGAGCGCTGGCCCTTA 36  
 RESULT 14  
 CG650062 64 bp mRNA linear GSS 02-OCT-2003  
 LOCUS CG650062

DEFINITION	ORIGIN	FEATURES	COMMENT
OSR406254 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSR406254, mRNA sequence.	Query Match Best Local Similarity 70.8%; Pred. No. 5.7e+04; Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	Location/Qualifiers 1..64 /organism="Mus musculus" /mol_type="mRNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OSR406254" /cell_type="embryonic stem cell" -/clone_idb="Mus musculus 129Sv/Ev"	Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11) Class: Gene Trap.
CG650062/cLOCUS DEFINITION OSR406254 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSR406254, mRNA sequence.	Accession CG650062 VERSION CG650062 KEYWORDS GSS.	Accession CG650062 VERSION CG650062 KEYWORDS GSS.	CG650062.1 GI:37473911 GSS.
REFERENCE AUTHORS	REFERENCE AUTHORS	REFERENCE AUTHORS	REFERENCE AUTHORS
ORGANISM	ORGANISM	ORGANISM	ORGANISM
Mus musculus (house mouse)	Mus musculus (house mouse)	Mus musculus (house mouse)	Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 64)	1 (bases 1 to 64)	1 (bases 1 to 64)	1 (bases 1 to 64)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, C.J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridele, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W., Jr., Kipp, P., Konhaufl, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.	Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, C.J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridele, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W., Jr., Kipp, P., Konhaufl, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.	Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, C.J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridele, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W., Jr., Kipp, P., Konhaufl, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.	Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, C.J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridele, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W., Jr., Kipp, P., Konhaufl, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention	Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention	Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention	Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

```

JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED      14610273
COMMENT      Contact: Zambrowicz BP
              OmniBank
              Lexicon Genetics Incorporated
              4000 Research Forest Drive, The Woodlands, TX 77381, USA
              Email: materials@lexgen.com
              Gene trap sequence tag generated by 3' RACE from mouse ES cells as
              described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
FEATURES
  source
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    /mol_type="mRNA"
    /strain="129Sv/Ev"
    /db_xref="taxon:10090"
    /clone="OST1406254"
    /cell_type="embryonic stem cell"
    /clone_lib="Mus musculus 129Sv/Ev"
  ORIGIN
    Query Match      58.4%; Score 14.6; DB 10; Length 64;
    Best Local Similarity 70.8%; Pred. No. 5.7e+04;
    Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
    2 ATTAGGGGCGCTGGCCCTTAATA 25
      ||| ||||| ||||| |||
    Db      51 ATTGAGGGCGCCGTCGCCNAAAAA 28
  
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Search completed: February 7, 2006, 12:06:36  
Job time : 3603 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 11:27:28 ; Search time 163 Seconds  
(without alignments)  
287.171 Million cell updates/sec

Title: US-10-613-390B-1

Perfect score: 25  
Sequence: 1 tattaaggagcctggcccttaata 25

Scoring table:  
IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3449518 seqs, 936177250 residues

Total number of hits satisfying chosen parameters: 5005474

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New:\*

- 1: /cgn2\_6/ptodata/2/pna/US06\_NEW COMB. seq.\*
- 2: /cgn2\_6/ptodata/2/pna/US06\_NEW COMB. seq.\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_NEW COMB. seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_NEW COMB. seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US09\_NEW COMB. seq.\*
- 6: /cgn2\_6/ptodata/2/pna/US10\_NEW COMB. seq.\*
- 7: /cgn2\_6/ptodata/2/pna/US10\_NEW COMB. seq.177an05.\*
- 8: /cgn2\_6/ptodata/2/pna/US10\_NEW COMB. seq.new.\*
- 9: /cgn2\_6/ptodata/2/pna/US11\_NEW COMB. seq.\*
- 10: /cgn2\_6/ptodata/2/pna/US11\_NEW COMB. seq.1.\*
- 11: /cgn2\_6/ptodata/2/pna/US11\_NEW COMB. seq.2.\*
- 12: /cgn2\_6/ptodata/2/pna/US60\_NEW COMB. seq.\*

Pred. No. is the number of results predicted by chance a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	15.6	62.4	60	US-11-130-645B-528520	Sequence 528520,
2	15.6	62.4	63	US-11-130-645B-150318	Sequence 150318,
3	15.6	62.4	64	US-11-130-645B-119663	Sequence 119663,
4	15.6	62.4	64	US-11-130-645B-139002	Sequence 139002,
5	15.6	62.4	64	US-11-130-645B-178751	Sequence 178751,
6	15.6	62.4	64	US-11-130-645B-236152	Sequence 236152,
7	15.6	62.4	64	US-11-130-645B-307585	Sequence 307585,
8	15.6	62.4	64	US-11-130-645B-333006	Sequence 333006,
9	15.6	62.4	64	US-11-130-645B-627039	Sequence 627039,
10	15.6	62.4	64	US-11-130-645B-688578	Sequence 688578,
11	15.6	61.6	64	US-11-130-645B-115601	Sequence 115601,
12	15.6	61.6	64	US-11-130-645B-235099	Sequence 235099,
13	15.4	61.6	64	US-11-130-645B-378454	Sequence 378454,
14	15.4	61.6	64	US-11-130-645B-378526	Sequence 378526,
15	15.4	61.6	64	US-11-130-645B-427234	Sequence 427234,
16	15.4	61.6	64	US-11-130-645B-459220	Sequence 459220,
17	15.4	61.6	64	US-11-130-645B-467734	Sequence 467734,
18	15.4	61.6	64	US-11-130-645B-569003	Sequence 569003,
19	15.2	60.8	63	US-11-130-645B-561328	Sequence 561328,
20	15.2	60.8	64	US-11-130-645B-165370	Sequence 165370,
21	15	60.0	64	US-11-130-645B-113088	Sequence 113088,

C 22	14.8	59.2	64	US-11-130-645B-217720	Sequence 217720,
C 23	14.8	59.2	64	US-11-130-645B-542527	Sequence 542527,
C 24	14.8	59.2	64	US-11-130-645B-604429	Sequence 604429,
C 25	14.8	59.2	64	US-11-130-645B-604559	Sequence 604559,
C 26	14.6	58.4	64	US-11-130-645B-333359	Sequence 333359,
C 27	14.6	58.4	64	US-11-130-645B-413655	Sequence 413655,
C 28	14.6	58.4	64	US-11-130-645B-483536	Sequence 483536,
C 29	14.6	58.4	64	US-11-130-645B-537703	Sequence 537703,
C 30	14.6	58.4	64	US-11-130-645B-661700	Sequence 661700,
C 31	14.6	58.4	64	US-11-130-645B-661823	Sequence 661823,
C 32	14.6	58.4	64	US-11-130-645B-661946	Sequence 661946,
C 33	14.6	58.4	64	US-11-130-645B-662069	Sequence 662069,
C 34	14.6	58.4	64	US-11-130-645B-662743	Sequence 662743,
C 35	14.6	58.4	64	US-11-130-645B-717754	Sequence 717754,
C 36	14.6	58.4	64	US-11-130-645B-738097	Sequence 738097,
C 37	14.4	57.6	62	US-11-130-645B-325028	Sequence 325028,
C 38	14.4	57.6	64	US-11-130-645B-112090	Sequence 112090,
C 39	14.4	57.6	64	US-11-130-645B-113739	Sequence 113739,
C 40	14.4	57.6	64	US-11-130-645B-117452	Sequence 117452,
C 41	14.4	57.6	64	US-11-130-645B-155510	Sequence 155510,
C 42	14.4	57.6	64	US-11-130-645B-179891	Sequence 179891,
C 43	14.4	57.6	64	US-11-130-645B-227807	Sequence 227807,
C 44	14.4	57.6	64	US-11-130-645B-367745	Sequence 367745,
C 45	14.4	57.6	64	US-11-130-645B-528942	Sequence 528942,

## ALIGNMENTS

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; Sequence 528520, Application US/11130645B  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: MICRONAS AND USES THEREOF  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645B  
; NUMBER OF SEQ ID NOS: 2005-05-16  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 528520  
; LENGTH: 60  
; TYPE: RNA  
; ORGANISM: hsa  
US-11-130-645B-528520

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Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TATTAAAGGCGCTGGCCCTTA 22  
Db 10 UAUUAAAGCACCUGACCUUA 31  
US-11-130-645B-150318  
; Sequence 150318, Application US/11130645B  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: MICRONAS AND USES THEREOF  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645B  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 150318  
; LENGTH: 63  
; TYPE: RNA  
; ORGANISM: hsa  
US-11-130-645B-150318  
Query Match 62.4%; Score 15.6; DB 11; Length 63;



/ CURRENT FILING DATE: 2005-05-16  
/ NUMBER OF SEQ ID NOS: 760616  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO: 333006  
/ LENGTH: 64  
/ TYPE: RNA  
/ ORGANISM: hsa  
US-11-130-645B-333006

Query Match 62.4%; Score 15.6; DB 11; Length 64;  
Best Local Similarity 59.1%; Pred. No. 3.1e+02;  
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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DB 25 UUAAGGGGCTGCGCCCTCAUCAU 46

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US-11-130-645B-627039

/ GENERAL INFORMATION:  
/ APPLICANT: ROSETTA GENOMICS LTD  
/ TITLE OF INVENTION: MICRORNAS AND USES THEREOF  
/ FILE REFERENCE: 06087.0202.CPUS13  
/ CURRENT APPLICATION NUMBER: US/11/130,645B  
/ CURRENT FILING DATE: 2005-05-16  
/ NUMBER OF SEQ ID NOS: 760616  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO: 627039  
/ LENGTH: 64  
/ TYPE: RNA  
/ ORGANISM: hsa  
US-11-130-645B-627039

Query Match 62.4%; Score 15.6; DB 11; Length 64;  
Best Local Similarity 59.1%; Pred. No. 3.1e+02;  
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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/ GENERAL INFORMATION:  
/ APPLICANT: ROSETTA GENOMICS LTD  
/ TITLE OF INVENTION: MICRORNAS AND USES THEREOF  
/ FILE REFERENCE: 06087.0202.CPUS13  
/ CURRENT APPLICATION NUMBER: US/11/130,645B  
/ CURRENT FILING DATE: 2005-05-16  
/ NUMBER OF SEQ ID NOS: 760616  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO: 688578  
/ LENGTH: 64  
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/ ORGANISM: hsa  
US-11-130-645B-688578

Query Match 62.4%; Score 15.6; DB 11; Length 64;  
Best Local Similarity 59.1%; Pred. No. 3.1e+02;  
Matches 13; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 TTAAGGGGCTGCGCCCTTAAT 24  
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RESULT 11  
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/ GENERAL INFORMATION:  
/ APPLICANT: ROSETTA GENOMICS LTD  
/ TITLE OF INVENTION: MICRORNAS AND USES THEREOF  
/ FILE REFERENCE: 06087.0202.CPUS13  
/ CURRENT APPLICATION NUMBER: US/11/130,645B  
/ CURRENT FILING DATE: 2005-05-16  
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/ SOFTWARE: PatentIn version 3.3  
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/ TYPE: RNA  
/ ORGANISM: hsa  
US-11-130-645B-115601

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Best Local Similarity 94.1%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 19 AAGGGGCTGCGCCCTT 3

RESULT 12  
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/ GENERAL INFORMATION:  
/ APPLICANT: ROSETTA GENOMICS LTD  
/ TITLE OF INVENTION: MICRORNAS AND USES THEREOF  
/ FILE REFERENCE: 06087.0202.CPUS13  
/ CURRENT APPLICATION NUMBER: US/11/130,645B  
/ CURRENT FILING DATE: 2005-05-16  
/ NUMBER OF SEQ ID NOS: 760616  
/ SOFTWARE: PatentIn version 3.3  
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/ LENGTH: 64  
/ TYPE: RNA  
/ ORGANISM: hsa  
US-11-130-645B-235099

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Best Local Similarity 94.1%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 19 AAGGGGCTGCGCCCTT 3

RESULT 13  
US-11-130-645B-378454/c  
/ GENERAL INFORMATION:  
/ APPLICANT: ROSETTA GENOMICS LTD  
/ TITLE OF INVENTION: MICRORNAS AND USES THEREOF  
/ FILE REFERENCE: 06087.0202.CPUS13  
/ CURRENT APPLICATION NUMBER: US/11/130,645B  
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/ SOFTWARE: PatentIn version 3.3  
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/ LENGTH: 64  
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/ ORGANISM: hsa  
US-11-130-645B-378454

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Best Local Similarity 94.1%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAGGGGCTGCGCCCTT 21  
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## RESULT 14

US-11-130-645B-378526/c  
; Sequence 378526, Application US/11130645B  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: MICRONAS AND USES THEREOF  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645B  
; CURRENT FILING DATE: 2005-05-16  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 378526  
; LENGTH: 64  
; TYPE: RNA  
; ORGANISM: hsa  
US-11-130-645B-378526

Query Match 61.6%; Score 15.4; DB 11; Length 64;  
Best Local Similarity 94.1%; Pred. No. 4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCTT 21  
|||||

Db 22 AAGGGGCTGGCCCTT 6  
|||||

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US-11-130-645B-427234/c  
; Sequence 427234, Application US/11130645B  
; GENERAL INFORMATION:  
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; TITLE OF INVENTION: MICRONAS AND USES THEREOF  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645B  
; CURRENT FILING DATE: 2005-05-16  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 427234  
; LENGTH: 64  
; TYPE: RNA  
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US-11-130-645B-427234

Query Match 61.6%; Score 15.4; DB 11; Length 64;  
Best Local Similarity 94.1%; Pred. No. 4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAGGGGCTGGCCCTT 21  
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Db 22 AAGGGGCTGGCCCTT 6  
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Search completed: February 7, 2006, 12:30:41  
Job time : 164 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 11:18:34 (Search time 3629 Seconds  
(without alignments)  
380.901 Million cell updates/sec

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Perfect score: 25  
Sequence: 1 tattaaaggcgccctgcccccttaata 25

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 91431180

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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2	25	100.0	25	53 PCT-US03-20696-7	Sequence 7, Appli
3	23.4	93.6	25	1 PCT-US03-20696-7	Sequence 7, Appli
4	23.4	93.6	25	53 US-10-613-390B-1	Sequence 1, Appli
5	17.4	69.6	25	62 US-10-809-189-116728	Sequence 1, Appli
6	17.2	68.8	25	38 US-09-956-584A-36654	Sequence 36654, A
7	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
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9	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
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11	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
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27	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
28	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
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31	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
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33	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
34	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
35	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
36	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
37	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
38	17.2	68.8	25	38 US-09-956-604A-22327	Sequence 22327, A
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#### SUMMARIES



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26 15.8 63.2 21 49 US-10-310-914A-621697 Sequence 621697, A
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42 15.8 63.2 25 66 US-11-036-317-374272 Sequence 374272, A
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44 15.8 63.2 25 78 US-60-353-987-621452 Sequence 621452, A
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## ALIGNMENTS

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RESULT 1
PCT-US03-20696-7
; Sequence 7, Application PC/TUS0320696
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning, Inc.
; APPLICANT: Zhifang Zhu
; APPLICANT: Yuliang Cui
; APPLICANT: Qingqing Ding
; APPLICANT: Li Li
; APPLICANT: Zhi Wang
; TITLE OF INVENTION: Oligonucleotides for Treating
; Proliferative Disorders
; FILE REFERENCE: 13552PCT
; CURRENT APPLICATION NUMBER: PCT/US03/20696
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/400,137
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_signal
; LOCATION: (0)...(0)
; OTHER INFORMATION: found in any organism
; FEATURE:
; OTHER INFORMATION: found in any organism
PCT-US03-20696-7

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Query Match 100.0%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TATTAAGGGGCGCTGGCCCTTAATA 25

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; Sequence 1, Application US/10613390B
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning Inc
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders

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; FILE REFERENCE: 60/400,137
; CURRENT APPLICATION NUMBER: US/10/613,390B
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10/613390
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic primer
US-10-613-390B-1
Query Match 100.0%; Score 25; DB 53; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TATTAAGGGGCGCTGGCCCTTAATA 25

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RESULT 3
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; Sequence 7, Application PC/TUS0320696
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning, Inc.
; APPLICANT: Zhifang Zhu
; APPLICANT: Yuliang Cui
; APPLICANT: Qingqing Ding
; APPLICANT: Li Li
; APPLICANT: Zhi Wang
; TITLE OF INVENTION: Oligonucleotides for Treating
; Proliferative Disorders
; FILE REFERENCE: 13552PCT
; CURRENT APPLICATION NUMBER: PCT/US03/20696
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/400,137
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_signal
; LOCATION: (0)...(0)
; OTHER INFORMATION: found in any organism
; FEATURE:
; OTHER INFORMATION: found in any organism
PCT-US03-20696-7

```

```

Query Match 93.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TATTAAGGGGCGCTGGCCCTTAATA 25
Db 25 TATTAAGGGGCGAGGCCCTTAATA 1

```

```

RESULT 4
US-10-613-390B-1/c
; Sequence 1, Application US/10613390B
; GENERAL INFORMATION:
; APPLICANT: Gene Cloning Inc
; TITLE OF INVENTION: Oligonucleotides for Treating Proliferative Disorders
; FILE REFERENCE: 60/400,137
; CURRENT APPLICATION NUMBER: US/10/613,390B
; CURRENT FILING DATE: 2003-07-03

```

PRIOR APPLICATION NUMBER: 10/613390  
PRIOR FILING DATE: 2003-07-03  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patent version 3.2  
SEQ ID NO 1  
LENGTH: 25  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic primer  
US-10-613-390B-1

Query Match 93.6%; Score 23.4; DB 53; Length 25;  
Best Local Similarity 96.0%; Pred. No. 25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TATTAAAGGGCGCTGGCCCTTAATA 25  
DB 25 TATTAAAGGGCGCGAGCCCTTAATA 1

RESULT 5  
US-10-809-189-116728/c  
Sequence 116728, Application US/10809189  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: Aftymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/10/809,189  
CURRENT FILING DATE: 2004-03-25  
PRIOR APPLICATION NUMBER: US/09/396,196  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: PasteSeq for Windows Version 4.0  
SEQ ID NO 116728  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-10-809-189-116728

Query Match 69.6%; Score 17.4; DB 62; Length 25;  
Best Local Similarity 94.7%; Pred. No. 9.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AGGGGCTGGCGCCCTTAAT 24  
DB 25 AGGGGCTGGCGACCTTAAT 7

RESULT 6  
US-09-956-584A-366654/c  
Sequence 366654, Application US/09956584A  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Genetic Analysis of Mouse  
FILE REFERENCE: 3115.1  
CURRENT APPLICATION NUMBER: US/09/956,584A  
CURRENT FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: 60/234,017  
PRIOR FILING DATE: 2000-09-20  
NUMBER OF SEQ ID NOS: 605887  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 366654  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-956-584A-366654

Query Match 68.8%; Score 17.2; DB 38; Length 25;  
Best Local Similarity 86.4%; Pred. No. 1.2e+04;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 TTAAGGGCGCTGGCCCTTAAT 24  
DB 23 TTCAAGGGCGCTGGCTTCAT 2

RESULT 7  
US-09-956-604-22327/c  
Sequence 22327, Application US/09956604  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli  
FILE REFERENCE: 3117.1  
CURRENT APPLICATION NUMBER: US/09/956,604  
CURRENT FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: 60/234,049  
PRIOR FILING DATE: 2000-09-19  
NUMBER OF SEQ ID NOS: 141629  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 22327  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-956-604-22327

Query Match 68.8%; Score 17.2; DB 38; Length 25;  
Best Local Similarity 86.4%; Pred. No. 1.2e+04;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TATTAAAGGGCGCTGGCCCTTA 22  
DB 24 TATTAAAGGGCGCTGGCTTCA 3

RESULT 8  
US-09-956-604A-22327/c  
Sequence 22327, Application US/09956604A  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli  
FILE REFERENCE: 3117.1  
CURRENT APPLICATION NUMBER: US/09/956,604A  
CURRENT FILING DATE: 2001-09-19  
PRIOR APPLICATION NUMBER: 60/234,049  
PRIOR FILING DATE: 2000-09-19  
NUMBER OF SEQ ID NOS: 141629  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 22327  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-956-604A-22327

Query Match 68.8%; Score 17.2; DB 38; Length 25;  
Best Local Similarity 86.4%; Pred. No. 1.2e+04;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TATTAAAGGGCGCTGGCCCTTA 22  
DB 24 TATTAAAGGGCGCTGGCTTCA 3

RESULT 9  
US-09-956-604B-22327/c  
Sequence 22327, Application US/09956604B  
GENERAL INFORMATION:  
APPLICANT: Miltmann, Michael  
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli  
FILE REFERENCE: 3117.1  
CURRENT APPLICATION NUMBER: US/09/956,604B

```

CURRENT FILING DATE : 2001-09-19
PRIORITY APPLICATION NUMBER : 60/7234,049
PRIOR FILING DATE : 2000-09-19
NUMBER OF SEQ ID NOS : 141629
SOFTWARE : Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 22327
LENGTH : 25
TYPE : DNA
ORGANISM : Escherichia coli
US-09-956-604B-22327

Query Match      68.8% ; Score 17.2; DB 38; Length 25;
Best Local Similarity 86.4% ; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY      1 TATTAAGGGGCTGCCCCCTTA 22
Db       24 TATTACGGGCGCTGTGCCTTA 3

```

```

RESULT 10
US-60-234-049-56273/c
: Sequence 56273, Application US/60234049
: GENERAL INFORMATION:
: APPLICANT: Miltmann, Michael
: APPLICANT: Affymetrix, Inc.
: TITLE OF INVENTION: Methods of Genetic Analysis of
: TITLE OF INVENTION: Escherichia coli
: FILE REFERENCE: 3117
: CURRENT APPLICATION NUMBER: US/60/234,049
: CURRENT FILING DATE: 2000-09-19
: NUMBER OF SEQ ID NOS: 141629
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 56273
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Escherichia coli
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: GenBank U00096
: US-60-234-049-56273

```

Query Match	68.8%	Score 17.2;	DB 77;	Length 25;
Best Local Similarity	86.4%	Pred. No. 1.2e+04;		
Matches 19; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 TATTAGGGCGCTGCCCCCTTA 22  
||| ||| ||| ||| |||  
Db 24 TATTAACGGGCTTGGTCCCTTA 3

```

RESULT 11
US-09-498-485A-1998
; Sequence 1998, Application US/09498485A
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 46
; FILE REFERENCE: PO46
; CURRENT APPLICATION NUMBER: US/09/498,485A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/118,775
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 8166
; SEQ ID NO 1998
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (39)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (61)
; OTHER INFORMATION: n equals a,t,g, or c

```

```

: NAME/KEY: misc_feature
: LOCATION: (66)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (73)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (98)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-498-485A-1998

Query Match      68.0%; Score 17; DB 24; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy      1 TATTAAAGGGGCTTGCGCCCTTAATA 25
      |||||
db      9 TGTAAAGGGGCTTGCGCTTGAAA 33

```

```

RESULT 12
US-09-912-293-44099
: Sequence 44099, Application US/09912293
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al.
: TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
: FILE REFERENCE: PO-100
: CURRENT FILING DATE: 2001-07-26
: PRIOR APPLICATION NUMBER: 08/103,744
: PRIOR FILING DATE: 1993-08-09
: PRIOR APPLICATION NUMBER: 09/249,651
: PRIOR FILING DATE: 1999-02-12
: PRIOR APPLICATION NUMBER: 08/104,507
: PRIOR FILING DATE: 1993-08-09
: PRIOR APPLICATION NUMBER: 08/196,363
: PRIOR FILING DATE: 1994-02-15
: PRIOR APPLICATION NUMBER: 09/859,490
: PRIOR FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: 08/196,362
: PRIOR FILING DATE: 1994-02-15
: PRIOR APPLICATION NUMBER: 08/221,623
: PRIOR FILING DATE: 1994-03-31
: PRIOR APPLICATION NUMBER: 08/220,691
: PRIOR FILING DATE: 1994-03-31
: PRIOR APPLICATION NUMBER: 09/741,830
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 09/613,155
: PRIOR FILING DATE: 2001-03-21
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 244538
: SEQ ID NO 44099
: LENGTH: 99
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (39)..(39)
: OTHER INFORMATION: n is equal to a,t,g, or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (61)..(61)
: OTHER INFORMATION: n is equal to a,t,g, or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (66)..(66)
: OTHER INFORMATION: n is equal to a,t,g, or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (73)..(73)
: OTHER INFORMATION: n is equal to a,t,g, or c
: FEATURE:
: NAME/KEY: misc_feature

```

LOCATION: (98)..(98)  
OTHER INFORMATION: n is equal to a,t,g, or c  
US-09-912-293-44099

Query Match 68.0%; Score 17; DB 35; Length 99;  
Best Local Similarity 80.0%; Pred. No. 1.6e+04;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TATTAGGGGCGCCCTTAATA 25  
Db 9 TATTAGGGGCGCCCTTAATA 33

## RESULT 13

US-09-498-485A-4160  
Sequence 4160, Application US/09498485A  
GENERAL INFORMATION:  
APPLICANT: Rosen, et. al.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 46  
FILE REFERENCE: PO46  
CURRENT APPLICATION NUMBER: US/09/498,485A  
CURRENT FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/118,775  
PRIOR FILING DATE: 1999-02-05  
NUMBER OF SEQ ID NOS: 8166  
SEQ ID NO 4160

LENGTH: 99  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (8)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (19)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (25)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (26)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (27)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (29)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (71)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (82)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (92)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-498-485A-4160

Query Match 65.6%; Score 16.4; DB 24; Length 99;  
Best Local Similarity 94.4%; Pred. No. 2.8e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TATTAGGGGCGCCCTTAATA 18  
Db 43 TATTAGGGGCGCCCTTAATA 60

## RESULT 14

US-09-498-485A-4160/c  
Sequence 4160, Application US/09498485A  
GENERAL INFORMATION:  
APPLICANT: Rosen, et. al.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 46  
FILE REFERENCE: PO46  
CURRENT APPLICATION NUMBER: US/09/498,485A  
CURRENT FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/118,775  
PRIOR FILING DATE: 1999-02-05  
NUMBER OF SEQ ID NOS: 8166  
SEQ ID NO 4160

LENGTH: 99  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (8)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (19)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (25)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (26)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (27)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (29)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (71)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (82)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc\_feature  
LOCATION: (92)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-498-485A-4160

Query Match 65.6%; Score 16.4; DB 24; Length 99;  
Best Local Similarity 94.4%; Pred. No. 2.8e+04;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 GGGCGGCGCCCTTAATA 25  
Db 60 GGGCGGCGCCCTTAATA 43

## RESULT 15

US-09-912-293-117317  
Sequence 117317, Application US/09912293  
GENERAL INFORMATION:  
APPLICANT: Rosen, et. al.  
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100  
FILE REFERENCE: PO-100  
CURRENT APPLICATION NUMBER: US/09/912,293  
CURRENT FILING DATE: 2001-07-26  
PRIOR APPLICATION NUMBER: 08/103,744  
PRIOR FILING DATE: 1993-08-09  
PRIOR APPLICATION NUMBER: 09/249,651  
PRIOR FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: 08/104,507  
PRIOR FILING DATE: 1993-08-09  
PRIOR APPLICATION NUMBER: 08/196,363  
PRIOR FILING DATE: 1994-02-15  
PRIOR APPLICATION NUMBER: 09/859,490  
PRIOR FILING DATE: 2001-05-18  
PRIOR APPLICATION NUMBER: 08/196,362  
PRIOR FILING DATE: 1994-02-15  
PRIOR APPLICATION NUMBER: 08/221,623  
PRIOR FILING DATE: 1994-03-31

```

; PRIOR APPLICATION NUMBER: 08/220,691
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 09/741,830
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/813,155
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 244538
; SEQ ID NO 117317
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)..(27)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (71)..(71)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (82)..(82)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92)..(92)
; OTHER INFORMATION: n is equal to a,t,g, or c
; US-09-912-293-117317

```

```

Query Match          65.6%; Score 16.4; DB 35; Length 99;
Best Local Similarity 94.4%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 TATTAGGGGCGCTGGCCC 18
         |||||
Db      43 TATTAGGGGCGCGGCC 60

```

Search completed: February 7, 2006, 12:27:52  
Job time : 3631 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 10:53:05 (Search time 272 Seconds

(without alignments)  
612.564 Million cell updates/sec

Title: US-10-613-390B-1

Perfect score: 25

Sequence: 1 tatcaaggcgctgcgcctccttaata 25

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 5288460

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_21:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	12	ADK67857 Transcrip
2	23.4	93.6	25	12	ADK67857 Transcrip
3	15.8	63.2	51	14	AA130340 Human SNP
4	15.4	61.6	50	4	AA131509 Human SNP
5	15.4	61.6	50	4	AA131507 Human SNP
6	15	60.0	90	14	ACL62385 Human col
7	14.4	57.6	70	2	AA171443 Human col
8	14.2	56.8	31	3	AA178645 Human gen
9	14.2	56.8	49	2	AA069655 Human ade
10	14.2	56.8	49	2	AA069655 Human ade
11	14.2	56.8	49	2	AA164117 Human ade
12	14.2	56.8	49	2	AA164117 Human ade
13	14.2	56.8	49	2	AA17405 Test sequ
14	14.2	56.8	49	2	AA17405 Test sequ
15	14.2	56.8	49	6	ABK82896 DNA bindi
16	14.2	56.8	49	6	ABK82896 DNA bindi
17	14.2	56.8	49	12	ADK80435 Duplex ol
18	14.2	56.8	49	12	ADK80435 Duplex ol
19	14.2	56.8	51	4	AA130340 Human SNP

C	20	14	56.0	18	2	AAK04573
C	21	14	56.0	63	2	AAZ11454
C	22	13.8	55.2	21	10	ADD94048
C	23	13.8	55.2	21	10	ADD94058
C	24	13.8	55.2	25	9	ACK17136
C	25	13.8	55.2	25	9	ACK17137
C	26	13.8	55.2	37	12	ADK17981
C	27	13.8	55.2	37	12	ADK17982
C	28	13.8	55.2	37	12	ADJ53933
C	29	13.8	55.2	37	12	ADJ53934
C	30	13.8	55.2	45	8	ABT34022
C	31	13.8	55.2	50	4	AA131509
C	32	13.8	55.2	51	4	AA131507
C	33	13.8	55.2	51	4	AA128172
C	34	13.8	55.2	61	3	AA11080
C	35	13.8	55.2	83	4	AA127785
C	36	13.8	55.2	83	4	ABA76096
C	37	13.8	55.2	83	4	AAK24770
C	38	13.8	55.2	83	6	ABE24246
C	39	13.6	54.4	22	10	ADJ95320
C	40	13.6	54.4	30	14	ADZ11539
C	41	13.6	54.4	32	5	AA161993
C	42	13.6	54.4	42	6	ABL95768
C	43	13.6	54.4	49	10	ADB67044
C	44	13.6	54.4	68	12	ADM87895
C	45	13.6	54.4	70	14	ADZ27716

## ALIGNMENTS

RESULT 1  
ADK67857 standard; DNA; 25 BP.

ADK67857;

06-MAY-2004 (first entry)

Transcription activator-binding oligonucleotide (oligo #2).

Cytostatic; lung cancer; melanoma; leukaemia; gene therapy; ss.

Synthetic.

Key Location/Qualifiers

FT TATA\_signal 1..6

FT GC\_signal 7..12

FT GC\_signal /\*tag= b

PD WO2004012654-A2.

PD 12-FEB-2004.

PF 30-JUN-2003; 2003WO-US020696.

PR 01-AUG-2002; 2002US-0400137P.

PA (GENE-) GENE CLONING INC.

PI Zhu Z, Cui Y, Ding Q, Li L, Wang Z;

DR WPI; 2004-156997/15.

PT Treating a proliferative disorder in a subject comprises administering a

PT proliferation-inhibiting amount of a single-stranded oligonucleotide

PT capable of binding to one or more DNA-binding proteins or RNA primers in

PT the subject.

PS Example 21; SEQ ID NO 7; 36pp; English.

PS The present sequence is that of oligo #2, a 25-mer single-stranded



CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
CC  
SQ Sequence 51 BP; 14 A; 16 C; 18 G; 3 T; 0 U; 0 Other;  
Query Match Score 15.8; DB 4; Length 51;  
Best Local Similarity 89.5%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 TATTAGGGGCGCTGGCCCC 19  
31 TTTTAGGGGCGCTGGCCCC 13  
Db  
RESULT 4  
AAL31509/c  
ID AAL31509 standard; DNA; 50 BP.  
XX  
AC AAL31509;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #4717.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinase; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US035498.  
XX  
PR 28-DEC-1999; 99US-0173419P.  
XX  
PR 27-DEC-2000; 2000US-00173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI: 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX  
PS Claim 1; Page 2743; 4143pp; English.  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinasins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms

CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
CC  
SQ Sequence 50 BP; 8 A; 17 C; 19 G; 6 T; 0 U; 0 Other;  
Query Match Score 15.4; DB 4; Length 50;  
Best Local Similarity 94.1%; Pred. No. 8.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 4 TTAGGGGCGCTGGCCCCCT 20  
18 TTAGGGGCGCTGGCCACT 2  
Db  
RESULT 5  
AAL31507/c  
ID AAL31507 standard; DNA; 50 BP.  
XX  
AC AAL31507;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #4715.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinase; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US035498.  
XX  
PR 28-DEC-1999; 99US-0173419P.  
XX  
PR 27-DEC-2000; 2000US-00173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI: 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX  
PS Claim 1; Page 2743; 4143pp; English.  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinasins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms



XX SQ Sequence 50 BP; 8 A; 14 C; 22 G; 6 T; 0 U; 0 Other;  
Query Match 61.6%; Score 15.4; DB 4; Length 50;  
Best Local Similarity 94.1%; Pred. No. 8.7e+2;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TAAAGGGGCTGGCCCT 20  
DB 44 TAAAGGGGCTGGCCACT 28  
RESULT 6  
ACL62385  
ID ACL62385 standard; cDNA; 90 BP.  
XX  
XX  
AC ACL62385;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX Human colon cancer differentially expressed polynucleotide, SEQ ID:8520.  
XX  
XX Differential expression; diagnosis; therapy; drug screening; cancer;  
XX  
XX neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;  
XX  
XX ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200500087-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 13-MAY-2004; 2004WO-US015421.  
XX  
XX 03-JUN-2003; 2003US-0475872P.  
XX  
XX (CHIR) CHIRON CORP.  
XX  
XX Randazzo F, Moler E, Escobedo J, Garcia PD;  
XX  
XX WPI; 2005-075421/08.  
XX  
XX  
XX New isolated polynucleotides, which are differentially expressed in colon  
XX  
XX cancer cell, useful for treating cancer, e.g. colon cancer, breast  
XX  
XX cancer, or pancreatic cancer.  
XX  
XX  
XX Claim 1; SEQ ID NO 8520; 97pp; English.  
XX  
XX The invention relates to 9672 polynucleotides (ACL6386-ACL63537) which  
XX  
XX are differentially expressed in colon cancer cells. The invention also  
XX  
XX relates to vectors and host cells comprising a differentially expressed  
XX  
XX polynucleotide of the invention; a method for detecting a cancerous cell  
XX  
XX by detection of a gene product of the polynucleotides; a method for  
XX  
XX inhibiting a cancerous phenotype of a cell by inhibiting a gene product  
XX  
XX of the polynucleotides; a method of treating an individual with cancer by  
XX  
XX administration of a modulator of a gene product of the polynucleotides;  
XX  
XX and an isolated antibody that specifically binds to a polypeptide encoded  
XX  
XX by one of the 9672 polynucleotides. The polynucleotides, polypeptides,  
XX  
XX antibodies, and methods are useful for the detection of cancerous cells;  
XX  
XX for the diagnosis, prognosis and management of cancer; for the  
XX  
XX identification of agents that modulate the phenotype of cancerous cells;  
XX  
XX for the identification of therapeutic targets for cancer chemotherapy;  
XX  
XX and for the treatment of cancer, especially colon cancer and metastasized  
XX  
XX colon cancer, but also breast or pancreatic cancer. The polynucleotides  
XX  
XX are also useful as a source of probes or primers for use in diagnostic  
XX  
XX methods. The differentially expressed polynucleotides or their encoded  
XX  
XX proteins can additionally be used as vaccines to modulate primary immune  
XX  
XX responses for the prevention or treatment of cancer. The present sequence  
XX  
XX represents a specifically claimed polynucleotide which is differentially  
XX  
XX expressed in colon cancer. Note: The sequence data for this patent did  
XX  
XX not form part of the printed specification, but was obtained in  
XX  
XX electronic format directly from WIPO at  
XX  
XX ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 90 BP; 21 A; 32 C; 22 G; 15 T; 0 U; 0 Other;  
Query Match 60.0%; Score 15; DB 14; Length 90;  
Best Local Similarity 78.3%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 3 TTAAGGGGCTGGCCCTTAATA 25  
DB 35 TTAAGGGGCTGGCCCTTAACA 57  
RESULT 7  
AAT71443/c  
ID AAT71443 standard; DNA; 70 BP.  
XX  
XX  
AC AAT71443;  
XX  
XX  
DT 01-AUG-1997 (first entry)  
XX  
XX  
DE Glioblastoma U251 cell line ligand GBI.86.  
XX  
XX  
XX Ligand; glioblastoma; brain; tumour; SELEX; in vivo; imaging;  
XX  
XX systematic evolution of ligands by exponential enrichment; cancer;  
XX  
XX drug delivery; cell line; ss.  
XX  
XX  
XX Synthetic.  
XX  
XX  
XX WO9634875-A1.  
XX  
XX  
XX 07-NOV-1996.  
XX  
XX  
XX 01-MAY-1996; 96WO-US006060.  
XX  
XX  
XX 03-MAY-1995; 95US-00433585.  
XX  
XX 03-MAY-1995; 95US-00434001.  
XX  
XX 03-MAY-1995; 95US-00434425.  
XX  
XX 03-MAY-1995; 95US-00437667.  
XX  
XX  
XX (NEXS-) NEXSTAR PHARM INC.  
XX  
XX (UYRE-) UNIV RES CORP.  
XX  
XX  
XX Jensen KB, Chen H, Morris KN, Stephens A, Gold L;  
XX  
XX WPI; 1996-506092/50.  
XX  
XX  
XX Identifying nucleic acid ligands for tissues - by contacting candidate  
XX  
XX mixt. of nucleic acids with tissue and enriching for increased affinity  
XX  
XX nucleic acids.  
XX  
XX  
XX Claim 22; Page 70; 110pp; English.  
XX  
XX The present sequence is a single stranded DNA ligand to the human brain  
XX  
XX tumor derived, glioblastoma U251 cell line, prepared by systematic  
XX  
XX evolution of ligands by exponential enrichment (SELEX). A single stranded  
XX  
XX DNA pool was incubated with U251 cells, and the tighter binding sequences  
XX  
XX partitioned from the rest of the pool by filtering the reaction through  
XX  
XX nitrocellulose filters. Twenty rounds of selection were carried out,  
XX  
XX using a decreasing concentration of U251 cells as the SELEX progressed.  
XX  
XX ligands to glioblastoma cell lines can be used in vivo to image  
XX  
XX glioblastomas, and for the therapeutic localisation of the ligand or  
XX  
XX other attached therapeutic agents  
XX  
XX  
XX Sequence 70 BP; 11 A; 20 C; 14 G; 25 T; 0 U; 0 Other;  
QY  
DB 2 ATTAAGGGGCTGGCCCTTAATA 25  
60 AATAAGGGGCTGGAGCTTAACA 37

RESULT 8  
ID AAA78645 standard; DNA; 31 BP.  
XX  
AC AAA78645;  
XX  
DT 20-NOV-2000 (first entry)  
XX  
DE Human genomic DNA polymorphic site sequence tag SEQ ID NO:15.  
XX  
KW Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe;  
KW hybridisation; polymorphic site; forensic; paternity testing; medicine;  
KW phenotypic trait; genetic analysis; genetic mapping; ds.  
XX  
OS Homo sapiens.  
XX  
PN EP1024200-A2.  
XX  
PD 02-AUG-2000.  
XX  
PF 26-JAN-2000; 2000EP-00250023.  
XX  
PR 27-JAN-1999; 99US-00238402.  
XX  
PA (APFY-) APFYMETRIX INC.  
XX  
PI Pacil N, Shah N, Warrington JA;  
XX  
DR WPI; 2000-500198/45.  
XX  
PT Human genomic polymorphic nucleic acid segments, allele specific primers  
PT and probes, and methods of analysis, useful for e.g. forensics, paternity  
PT testing, genetic mapping.  
XX  
PS Claim 1; Page 5; 141pp; English.  
XX  
CC The present invention describes a nucleic acid segment of 10-100  
CC contiguous bases chosen from one of 632 fragments (AAA78631 to AAA79262),  
CC where the segment comprises a polymorphic site or an immediately adjacent  
CC base, or the complement of the segment. Also described are: (1) an allele  
CC -specific oligonucleotide that hybridises to a segment of the novelty;  
CC (2) an isolated nucleic acid comprising a sequence of the novelty where  
CC the polymorphic site within the sequence is occupied by a base other than  
CC the reference base indicated in the specification; and (3) analysing a  
CC nucleic acid, comprising obtaining a nucleic acid from an individual, and  
CC determining a base occupying any one of the polymorphic sites of the  
CC novelty. The nucleic acid segments and method can be used to analyse an  
CC individual's nucleic acid sequences for the presence of polymorphisms. The  
CC method can also be used to test for a disease phenotype and correlate the  
CC presence of the phenotype with a particular polymorphism. The presence of  
CC polymorphic sites are useful for, e.g. forensics, paternity testing,  
CC correlation of polymorphisms with phenotypic traits and for genetic  
CC mapping of phenotypic traits. AAA78631 to AAA79262 represent sequence  
CC tags of human genomic DNA fragments containing polymorphic sites. The  
CC base occupying the polymorphic site is indicated using IUPAC-IUB  
CC nomenclature  
XX  
SQ Sequence 31 BP; 3 A; 8 C; 8 G; 11 T; 0 U; 1 Other;  
XX  
QY Query Match 56.8%; Score 14.2; DB 3; Length 31;  
Best Local Similarity 76.2%; Pred. No. 3.3e+03;  
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
XX  
DB 1 TATTAGGCGGCTGCCCCCTT 21  
9 TCTTCAGRGGAGCTGCGTCTCTT 29  
XX  
RESULT 9  
ID AA069655 standard; DNA; 49 BP.  
XX

AC AA069655;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-MAR-1995 (first entry)  
XX  
DE Human adenosine deaminase gene, target region.  
XX  
KW DNA protein-binding assay; test sequence; screening sequence; promoter;  
KW target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9;  
KW transcription factor; TRID; ds.  
XX  
OS Synthetic.  
XX  
PN WO9414980-A1.  
XX  
PD 07-JUL-1994.  
XX  
PF 20-DEC-1993; 93WO-US012388.  
XX  
PR 23-DEC-1992; 92US-00996783.  
PR 17-SEP-1993; 93US-00123936.  
XX  
PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX  
PI Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;  
XX  
DR WPI, 1994-234711/28.  
XX  
PT Sequence-directed DNA-binding molecules - useful in pharmaceuticals and  
PT as molecular reagents.  
XX  
PS Claim 28; Page 414; 587pp; English.  
XX  
CC A DNA protein-binding assay is provided, useful for screening libraries  
CC of synthetic or biological cpds. for their ability to bind DNA test  
CC sequences. The assay is versatile in that any number of test sequences  
CC can be tested by placing the test sequence adjacent to a defined protein-  
CC binding screening sequence. Binding of mole. to these test sequences  
CC changes the binding characteristics of the protein mol. to its cognate  
CC binding sequence. When such a mol. binds the test sequence, the  
CC equilibrium of the DNA-protein complexes is disturbed, generating changes  
CC in the concentration of free DNA probe. One application of this method is  
CC to eucaryotic general transcription factors (e.g. TFIID), where the  
CC target region is typically selected from DNA sequences adjacent to the  
CC binding site for the eucaryotic transcription factor. Numerous exemplary  
CC test sequences are given: the sequences in AA069251-731 and AA069850  
CC correspond to promoter targets (typically, TATA box-contg. sites) for  
CC human genes and the sequences in AA069732-849 correspond to promoter  
CC targets for viral genes. The test sequences may also be randomly  
CC generated. DNA:protein interaction may be used for screening purposes,  
CC e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see  
CC AA069851-52, AA069865 and AA069891). (updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;  
XX  
QY Query Match 56.8%; Score 14.2; DB 2; Length 49;  
Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
DB 7 GGGGCTTGGGCCCCCTTAATA 25  
10 GGGGCCCGGCCCGCCCTTAAGA 28  
XX  
RESULT 10  
ID AA069655 standard; DNA; 49 BP.  
XX  
AC AA069655;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-MAR-1995 (first entry)  
XX

DE	Human adenosine deaminase gene, target region.
XX	
XX	DNA protein-binding assay; test sequence; screening sequence; promoter;
KM	target; TATA box; Herpes Simplex Virus; HSV; origin of replication; Un9;
KW	transcription factor; TFIID; ds.
XX	
OS	Synthetic.
XX	
PM	W09414980-AL.
XX	
PD	07-JUL-1994.
XX	
PF	20-DEC-1993; 93WO-US012388.
XX	
PR	23-DEC-1992; 92US-00969783.
PR	17-SEP-1993; 93US-00123936.
XX	
PA	(GENE-) GENETLABS TECHNOLOGIES INC.
XX	
PI	Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;
XX	
DR	WPI. 1994-234711/28.
XX	
PT	Sequence-directed DNA-binding molecules - useful in pharmaceuticals and
XX	as molecular reagents.
PS	
XX	Claim 28; Page 414; 587pp; English.
XX	
CC	A DNA protein-binding assay is provided, useful for screening libraries
CC	of synthetic or biological cpds. for their ability to bind DNA test
CC	sequences. The assay is versatile in that any number of test sequences
CC	can be tested by placing the test sequence adjacent to a defined protein-
CC	binding screening sequence. Binding of mols. to these test sequences
CC	changes the binding characteristics of the protein mol. to its cognate
CC	binding sequence. When such a mol. binds the test sequence, the
CC	equilibrium of the DNA:protein complexes is disturbed, generating changes
CC	in the concentration of free DNA probe. One application of this method is
CC	to eucaryotic general transcription factors (e.g. TFIID), where the
CC	target region is typically selected from DNA sequences adjacent to the
CC	binding site for the eucaryotic transcription factor. Numerous exemplary
CC	test sequences are given: the sequences in AA069251-731 and AA069850
CC	correspond to promoter targets (typically, TATA box-contg. sites) for
CC	human genes and the sequences in AA069732-849 correspond to promoter
CC	targets for viral genes. The test sequences may also be randomly
CC	generated. DNA:protein interaction may be used for screening purposes,
CC	e.g. the Herpes Simplex Virus (HSV) origin of replication and Un9 (see
CC	AA069851-52, AA069865 and AA069891). (Updated on 25-MAR-2003 to correct
CC	PN field.)
XX	
SO	Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;
	Query Match 56.8%; Score 14.2; DB 2; Length 49;
	Best Local Similarity 84.2%; Pred. No. 3.5e+03;
	Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 TATTAAAGGGCCTGGCCCC 19
DB	28 TCTTAACGGCCCGGCGCC 10
RESULT 11	
ID	AAT64117
XX	AAT64117 standard; DNA; 49 BP.
XX	
AC	AAT64117;
XX	
DT	25-MAR-2003 (revised)
DT	17-MAR-1997 (first entry)
XX	
DE	Human adenosine deaminase gene TFIID binding site.
XX	
KW	Duplex DNA; target region; binding characteristic; DNA binding protein;

XX	TFIID; transcription factor; binding site; inhibition; enhance; cancer;
KW	inherited genetic disorder; da.
XX	
OS	Homo sapiens.
XX	
PN	US5578444-A.
XX	
PD	26-NOV-1996.
XX	
PF	20-DEC-1993; 93US-00171389.
XX	
PR	27-JUN-1991; 91US-00723618.
XX	
PR	23-DEC-1992; 92US-0096783.
XX	
PR	17-SEP-1993; 93US-00123936.
XX	
PA	(GENE-) GENELABS TECHNOLOGIES INC.
XX	
P1	FRY KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;
XX	
DR	WPI; 1997-020402/02.
XX	
PT	Altering binding characteristics of DNA binding proteins to duplex DNA -
XX	by attaching specific small cpd. to target region close to the protein's
PT	binding site, useful in treatment of viral disease, cancer etc.
XX	
PS	Claim 6; Col 305-306; 264pp; English.
XX	
CC	The sequences given in AAT63713-4312 represent duplex DNA's which act as
XX	target regions in the method of the invention. The method for altering
CC	the binding characteristics of a DNA-binding protein to duplex DNA
XX	comprises contacting the duplex DNA with a small molecule which binds
CC	sequence-specifically to a target region, where, when the small molecule
XX	is bound to the target region, it is adjacent to, but not overlapping by
CC	more than 4 bp, a binding site for a DNA-binding protein. The small
XX	molecule is added at a concentration effective to alter the binding of
CC	the DNA binding protein, pref. TFIID, to its binding site on the duplex
XX	DNA. The binding of the small molecule may inhibit or enhance the binding
CC	of the DNA-binding protein to its binding site. The compounds isolated
XX	using this method are potentially useful as therapeutic agents for
CC	treatment of any disease which involves a specific DNA sequence, e.g.
XX	cancer, or inherited genetic disorders etc. The method is suitable for
CC	screening large biological or chemical libraries and allows determination
XX	of sequence-specific and relative affinities of known DNA-binding agents
CC	for different DNA sequences. The design of these duplex DNA's allows a
XX	single DNA:protein interaction to be used for screening sequence-
CC	specific, or preferential, DNA binding proteins that recognise almost any
XX	possible sequence (see also AAT49539-74). (Updated on 25-MAR-2003 to
CC	correct PF field.)
XX	
SQ	Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;
XX	
Query Match	56.8%; Score 14.2; DB 2; Length 49;
Best Local Similarity	84.2%; Pred. NO. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
XX	
OY	7 GGGGCGTGGCCCTTAATA 25
XX	
DB	10 GGGGCGCGGCCCTTAAGA 28
XX	
RESULT 12	
AAT64117/c	
ID AAT64117 standard; DNA: 49 BP.	
XX	
AC AAT64117;	
XX	
DT 25-MAR-2003 (revised)	
DT 17-MAR-1997 (first entry)	
DE Human adenosine deaminase gene TFIID binding site.	
XX	
XX	Duplex DNA; target region; binding characteristic; DNA binding protein;
KW	TFIID; transcription factor; binding site; inhibition; enhance; cancer;

KW Inherited genetic disorder; ds.  
XX  
OS Homo sapiens.  
XX  
PN US5578444-A.  
XX  
PD 26-NOV-1996.  
XX  
PF 20-DEC-1993; 93US-00171389.  
XX  
PR 27-JUN-1991; 91US-00723618.  
PR 23-DEC-1992; 92US-0096783.  
PR 17-SEP-1993; 93US-00123936.  
XX  
PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX  
PI Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;  
XX  
DR WPI; 1997-020402/02.  
XX  
PT Altering binding characteristics of DNA binding proteins to duplex DNA -  
XX by attaching specific small cpd. to target region close to the protein's  
XX binding site, useful in treatment of viral disease, cancer etc.  
XX  
PS Claim 6; Col 305-306; 264pp; English.  
XX  
CC The sequences given in AAT63713-4312 represent duplex DNA's which act as  
CC target regions in the method of the invention. The method for altering  
CC the binding characteristics of a DNA-binding protein to duplex DNA  
CC comprises contacting the duplex DNA with a small molecule which binds  
CC sequence-specifically to a target region, where, when the small molecule  
CC is bound to the target region, it is adjacent to, but not overlapping by  
CC more than 4 bp, a binding site for a DNA-binding protein. The small  
CC molecule is added at a concentration effective to alter the binding of  
CC the DNA binding protein, pref. TFRID, to its binding site on the duplex  
CC DNA. The binding of the small molecule may inhibit or enhance the binding  
CC of the DNA-binding protein to its binding site. The compounds isolated  
CC using this method are potentially useful as therapeutic agents for  
CC treatment of any disease which involves a specific DNA sequence, e.g.  
CC cancer, or inherited genetic disorders etc. The method is suitable for  
CC screening large biological or chemical libraries and allows determination  
CC of sequence-specific and relative affinities of known DNA-binding agents  
CC for different DNA sequences. The design of these duplex DNA's allows a  
CC single DNA:protein interaction to be used for screening sequence-  
CC specific, or preferential, DNA binding proteins that recognise almost any  
CC possible sequence (see also AAT9359-74). (Updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 56.8%; Score 14.2; DB 2; Length 49;  
Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 1 TATTAGGCGGCTGGCCCC 19  
DB 28 TCTTAACGGCGCGCGCCCC 10  
XX  
RESULT 13  
AAAX17405  
ID AAAX17405 standard; DNA; 49 BP.  
XX  
AC AAAX17405;  
XX  
XX 06-MAY-1999 (first entry)  
XX  
DE Test sequence from human adenosine deaminase gene.  
XX  
KM Test sequence; DNA-binding molecule; screening sequence; human;  
XX nucleic acid amplification; target; viral; ds.  
XX  
OS Homo sapiens.

XX  
PN US5869241-A.  
XX  
PD 09-FEB-1999.  
XX  
PF 07-JUN-1995; 95US-00475228.  
XX  
PR 27-JUN-1991; 91US-00723618.  
PR 23-DEC-1992; 92US-0096783.  
PR 17-SEP-1993; 93US-00123936.  
PR 20-DEC-1993; 93US-00171389.  
XX  
PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX  
PI Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;  
XX  
DR WPI; 1999-152755/13.  
XX  
PT Determination of DNA sequence preference of a DNA-binding molecule -  
XX based on inhibition of binding of protein to oligonucleotide sequence  
XX attached to test sequence.  
XX  
PS Claim 3; Col 307-308; 270pp; English.  
XX  
CC Sequences AAAX17001 to AAAX17600 represent specifically claimed target test  
CC sequences that are used in the method of the invention of determining the  
CC DNA sequence preference of a DNA-binding molecule. The method comprises:  
CC (i) adding a test molecule and a DNA-binding protein to a mixture of  
CC duplex DNA test oligonucleotides, each of the test oligonucleotides  
CC having a test sequence adjacent to a screening sequence, where the  
CC screening sequence binds to the DNA-binding protein with a binding  
CC affinity that is independent of the DNA sequence of the test sequence,  
CC and where the mixture of duplex DNA test oligonucleotides includes  
CC several test sequences; (ii) incubating the test molecule, the mixture of  
CC duplex DNA test oligonucleotides and the DNA-binding protein for a time  
CC sufficient to permit binding of the test molecule to test sequences in  
CC the duplex DNA; (iii) separating unbound test oligonucleotides from test  
CC oligonucleotides bound to binding protein; (iv) amplifying the unbound  
CC test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating  
CC the amplified test oligonucleotides; and (vii) sequencing the isolated  
CC test oligonucleotides. Test sequences AAAX17001-X17481 and AAAX17600  
CC correspond to promoter targets for human genes and test sequences  
CC AAAX17482-X17599 correspond to promoter targets for viral genes  
XX  
SQ Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 56.8%; Score 14.2; DB 2; Length 49;  
Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 7 GGGGCTGGCGCCCTTAATN 25  
DB 10 GGGGCGCGCGCGCTTAAGA 28  
XX  
RESULT 14  
AAAX17405/C  
ID AAAX17405 standard; DNA; 49 BP.  
XX  
AC AAAX17405;  
XX  
XX 06-MAY-1999 (first entry)  
XX  
DE Test sequence from human adenosine deaminase gene.  
XX  
KM Test sequence; DNA-binding molecule; screening sequence; human;  
XX nucleic acid amplification; target; viral; ds.  
XX  
OS Homo sapiens.  
XX  
PN US5869241-A.  
XX  
PD 09-FEB-1999.

XX 07-JUN-1995; 95US-00475228.  
 XX 27-JUN-1991; 91US-00722618.  
 PR 23-DEC-1992; 92US-0096783.  
 PR 17-SEP-1993; 93US-00123936.  
 PR 20-DEC-1993; 93US-00171389.  
 XX (GENE-) GENELABS TECHNOLOGIES INC.  
 XX Fry KE, Turin LM, Andrews BM, Cantor CR, Edwards CA;  
 PI WPI; 1999-152755/13.  
 DR WPI; 1999-152755/13.  
 XX Determination of DNA sequence preference of a DNA-binding molecule -  
 PT based on inhibition of binding of protein to oligonucleotide sequence  
 PT attached to test sequence.  
 XX  
 PS Claim 3; Col 307-308; 270pp; English.  
 XX  
 CC Sequences AAX17001 to AAX17600 represent specifically claimed target test  
 CC sequences that are used in the method of the invention of determining the  
 CC DNA sequence preference of a DNA-binding molecule. The method comprises:  
 CC (i) adding a test molecule and a DNA-binding protein to a mixture of  
 CC duplex DNA test oligonucleotides, each of the test oligonucleotides  
 CC having a test sequence adjacent to a screening sequence, where the  
 CC screening sequence binds to the DNA-binding protein with a binding  
 CC affinity that is independent of the DNA sequence of the test sequence,  
 CC and where the mixture of duplex DNA test oligonucleotides includes  
 CC several test sequences; (ii) incubating the test molecule, the mixture of  
 CC duplex DNA test oligonucleotides and the DNA-binding protein for a time  
 CC sufficient to permit binding of the test molecule to test sequences in  
 CC the duplex DNA; (iii) separating unbound test oligonucleotides from test  
 CC oligonucleotides bound to binding protein; (iv) amplifying the unbound  
 CC test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating  
 CC the amplified test oligonucleotides; and (vii) sequencing the isolated  
 CC test oligonucleotides. Test sequences AAX17001-X17481 and AAX17600  
 CC correspond to promoter targets for human genes and test sequences  
 CC AAX17482-X17593 correspond to promoter targets for viral genes  
 CC  
 XX Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 56.8%; Score 14.2; DB 2; Length 49;  
 Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TATTAAAGGCGCTGCGCCC 19  
 DB 28 TCTTAACGGCGCGCGCCCC 10  
 RESULT 15  
 ABR82896  
 ID ABR82896 standard; DNA; 49 BP.  
 XX  
 AC ABR82896;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE DNA binding molecule screening method test sequence #405.  
 XX  
 XX DNA binding molecule screening; inhibition of transcription; infection;  
 KM human immunodeficiency virus; HIV; parasite; cancer; cardiovascular;  
 KM respiratory; gastrointestinal; endocrine; metabolic; rheumatic;  
 KM immunological; haematological; neurological; psychiatric; dermatological;  
 KM ophthalmological; musculo-skeletal; urogenital disorder; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US6384208-B1.  
 PN  
 XX 07-MAY-2002.  
 PD  
 XX

PF 15-JUL-1999; 99US-00354947.  
 XX 27-JUN-1991; 91US-00722618.  
 PR 23-DEC-1992; 92US-0096783.  
 PR 17-SEP-1993; 93US-00123936.  
 PR 20-DEC-1993; 93US-00171389.  
 PR 07-JUN-1995; 95US-00482080.  
 XX (GENE-) GENELABS TECHNOLOGIES INC.  
 XX Edwards CA, Cantor CR, Andrews BM, Turin LM, Fry KE;  
 PI WPI; 2002-442819/47.  
 DR WPI; 2002-442819/47.  
 XX  
 PT Decreasing transcriptional activity of genes for treating infections or  
 PT cancer, by administration of an agent that binds to two non-overlapping  
 PT regions of the gene.  
 XX  
 PS Example 15; SEQ ID NO 405; 98pp; English.  
 XX  
 CC The invention relates to a method of decreasing transcriptional activity  
 CC in a duplex deoxyribonucleic acid (DNA) template (T1) comprising  
 CC contacting (T1) with a binding agent comprising at least one small duplex  
 CC DNA-binding molecule (T2) coupled to at least one other small duplex-  
 CC binding molecule that binds to a non-overlapping region of target  
 CC sequence (TS). The method is useful for inhibiting transcription of a  
 CC range of disease-related genes for treating infections (by viruses, and  
 CC including human immunodeficiency virus, bacteria, fungi, protozoa and  
 CC parasites), cancer, cardiovascular, respiratory, gastrointestinal,  
 CC endocrine/metabolic, rheumatic/immunological, haematological,  
 CC neurological, psychiatric, dermatological, ophthalmological, musculo-  
 CC skeletal, genetic or urogenital disorders. The method provides sequence-  
 CC specific inhibition of transcription of pathological genes without  
 CC affecting transcription of cellular genes regulated by the same  
 CC transcription factor, and can be applied to regulation of any gene.  
 CC ABR82492-ABR83155 represent DNA binding molecule test sequences used in  
 CC the method of the invention  
 CC  
 XX Sequence 49 BP; 6 A; 16 C; 24 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 56.8%; Score 14.2; DB 6; Length 49;  
 Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 GGGGCTGGCGCCCTTAATA 25  
 DB 10 GGGGCGCGCGCCGCTTAAGA 28  
 Search completed: February 7, 2006, 13:57:24  
 Job time : 275 secs